

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: September 6, 2005, 09:10:34 ; Search time 138 Seconds  
(without alignments)  
9141.807 Million cell updates/sec

Title: US-08-790-043B-1  
Perfect score: 771  
Sequence: 1 ATGTTAAATCTTGAAACAA.....GATTCACGCATTAATAA 771

Scoring table: OLIGO NUC  
Gapop 60.0 , Gapext 60.0

Searched: 1202784 seqs, 818138359 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents NA:\*  
1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq.\*  
2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq.\*  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq.\*  
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5: /cgn2\_6/ptodata/1/ina/PTUS\_COMB.seq.\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	771	100.0	771	3	US-09-292-412-1
2	771	100.0	771	4	US-09-292-411A-1
3	506	65.6	916	4	US-10-138-701-5
4	437	56.7	704	4	US-08-956-171E-772
5	437	56.7	704	4	US-08-781-986A-772
6	63	8.2	587	4	US-08-956-171E-514
7	63	8.2	587	4	US-08-781-986A-514
8	30	3.9	39	4	US-10-089-740-1
9	30	3.9	39	4	US-09-292-411A-3
10	30	3.9	39	4	US-10-089-739-1
11	24	3.1	783	3	US-09-134-001C-1172
12	23	3.0	26	4	US-10-089-740-4
13	23	3.0	26	4	US-10-089-739-4
14	21	2.7	28	4	US-10-089-740-3
15	21	2.7	28	4	US-10-089-739-3
16	21	2.7	106929	4	US-09-949-016-12060
17	21	2.7	106929	4	US-09-949-016-16618
18	20	2.6	561	4	US-09-107-532A-3447
19	20	2.6	582	4	US-09-543-681A-2869
20	19	2.5	278866	4	US-09-949-016-13922
21	19	2.5	278866	4	US-09-949-016-13923
22	19	2.5	278866	4	US-09-949-016-13924
23	19	2.5	278866	4	US-09-949-016-13925
24	19	2.5	278866	4	US-09-949-016-13926
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27	19	2.5	278866	4	US-09-949-016-14701

28	19	2.5	278866	4	US-09-949-016-14702	Sequence 14702, A
29	19	2.5	278866	4	US-09-949-016-14703	Sequence 14703, A
30	19	2.5	1230025	4	US-09-198-452A-1	Sequence 1, Appli
31	19	2.5	1230230	4	US-09-438-185A-1	Sequence 1, Appli
C 32	18	2.3	483	4	US-09-583-110-1501	Sequence 1501, Ap
33	18	2.3	741	4	US-09-134-000C-60	Sequence 60, Appl
34	18	2.3	915	4	US-09-328-352-2076	Sequence 2076, Ap
C 35	18	2.3	1221	2	US-08-934-846-3	Sequence 3, Appli
C 36	18	2.3	1221	3	US-09-238-557-3	Sequence 3, Appli
C 37	18	2.3	1254	2	US-08-934-846-1	Sequence 1, Appli
C 38	18	2.3	1254	3	US-09-238-557-1	Sequence 1, Appli
C 39	18	2.3	1419	4	US-09-543-681A-443	Sequence 443, App
40	18	2.3	2304	4	US-09-328-352-487	Sequence 487, App
41	18	2.3	7853	4	US-09-949-016-14067	Sequence 14067, A
42	18	2.3	129127	4	US-09-949-016-13481	Sequence 13481, A
C 43	18	2.3	767677	4	US-09-949-016-12147	Sequence 12147, A
C 44	18	2.3	767677	4	US-09-949-016-17361	Sequence 17361, A
45	17	2.2	320	3	US-09-030-607-224	Sequence 224, App

ALIGNMENTS

RESULT 1  
US-09-292-412-1  
; Sequence 1, Application US/09292412  
; Patent No. 6432670  
; GENERAL INFORMATION:  
; APPLICANT: Payne, David  
; APPLICANT: Lonsdale, John  
; APPLICANT: Milner, Peter  
; APPLICANT: Pearson, Stewart  
; TITLE OF INVENTION: FAB I  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dechert Price & Rhoads  
; STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre  
; CITY: Philadelphia  
; STATE: PA  
; COUNTRY: US  
; ZIP: 19103  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: FastSeq for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/292,412  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/790,043  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Falk, Stephen T  
; REGISTRATION NUMBER: 36,795  
; REFERENCE/DOCKET NUMBER: GMS0005  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 215-994-2488  
; TELEFAX: 215-994-2222  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 771 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; US-09-292-412-1

Query Match 100.0%; Score 771; DB 3; Length 771;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 771; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 ATGTTAAATCTTGAAACAAACATATGTCATCGGGAATCGCTAATAAGCGTAGTATT 60
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Db 61 GCTTTTGGTGCCTAAAGTTTGTAGTCAATAGGTGCTAAATAGTATTACTTTACCGT 120
QY 121 AAAGAACGTAGCCGTAAAGAGCTTGAAAAATATTATAGAACAAATTAATCAACAGAGCG 180
Db 121 AAAGAACGTAGCCGTAAAGAGCTTGAAAAATATTATAGAACAAATTAATCAACAGAGCG 180
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Db 181 CACTTATATCAAAATTCATGTTCAAGCGATGAAGAGTTTAAATGGTTTTCAGCAAAAT 240
QY 241 GGTAAAGATGTTGGCAATATTGATGGTGATATCATTTCAATCGCATTTCTCTAATATGGAA 300
Db 241 GGTAAAGATGTTGGCAATATTGATGGTGATATCATTTCAATCGCATTTCTCTAATATGGAA 300
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Db 301 GACTTACGGGAGCGCTTTCTGAACTTCACGTGAAGGCTTCTTGTAGCTCAAGACATT 360
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Db 361 AGTTCTTACTCATTAACAATTTGGGCTCATGAAGCTTAAAAAATTAATGCCAGAGGTGGT 420
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Db 421 AGCATTGTTGCAACAAATATTAGTGGCGAAATTCGCAGTTCAAAATTTAATATGTGATG 480
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Db 481 GGTGTTGCTTAAAGCGAGCTTAGAACCAATGTTAAATATTAGCATTAGCTTAGTTCCT 540
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Db 721 GTTACAGGTGAAAAATATTTCATGTAGATAGCGGATTCACGCAATTAATAA 771
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## RESULT 2

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US-09-292-411A-1
; Sequence 1, Application US/09292411A
; Patent No. 6753172
; GENERAL INFORMATION:
; APPLICANT: Lonsdale, John
; APPLICANT: Milner, Peter
; APPLICANT: Payne, David
; APPLICANT: Pearson, Stewart
; TITLE OF INVENTION: Fabi
; FILE REFERENCE: GM50005-D1
; CURRENT APPLICATION NUMBER: US/09/292,411A
; CURRENT FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: US 08/790,043
; PRIOR FILING DATE: 1997-01-28
; PRIOR APPLICATION NUMBER: US 60/024,845
; PRIOR FILING DATE: 1996-08-26
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
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; LENGTH: 771
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-09-292-411A-1
Query Match 100.0%; Score 771; DB 4; Length 771;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 771; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGTTAAATCTTGAAAACAAAACATATGTCATCATGCGGAATCGCTAATAAGCGTAGTATT 60
Db 1 ATGTTAAATCTTGAAAACAAAACATATGTCATCATGCGGAATCGCTAATAAGCGTAGTATT 60
QY 61 GCTTTTGGTGCCTAAAGTTTGTAGATCAATAGGTGCTAAATAGTATTACTTTACCGT 120
Db 61 GCTTTTGGTGCCTAAAGTTTGTAGATCAATAGGTGCTAAATAGTATTACTTTACCGT 120
QY 121 AAAGAACGTAGCCGTAAAGAGCTTGAAAAAATATTATAGAACAAATTAATCAACAGAGCG 180
Db 121 AAAGAACGTAGCCGTAAAGAGCTTGAAAAAATATTATAGAACAAATTAATCAACAGAGCG 180
QY 181 CACTTATATCAAAATTCATGTTCAAGCGATGAAGAGTTTAAATGGTTTTCAGCAAAAT 240
Db 181 CACTTATATCAAAATTCATGTTCAAGCGATGAAGAGTTTAAATGGTTTTCAGCAAAAT 240
QY 241 GGTAAAGATGTTGGCAATATTGATGGTGATATCATTTCAATCGCATTTCTCTAATATGGAA 300
Db 241 GGTAAAGATGTTGGCAATATTGATGGTGATATCATTTCAATCGCATTTCTCTAATATGGAA 300
QY 301 GACTTACGGGAGCGCTTTCTGAAACTTCACGTGAAGGCTTCTTGTAGCTCAAGACATT 360
Db 301 GACTTACGGGAGCGCTTTCTGAAACTTCACGTGAAGGCTTCTTGTAGCTCAAGACATT 360
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Db 361 AGTTCTTACTCATTAACAATTTGGGCTCATGAAGCTTAAAAAATTAATGCCAGAGGTGGT 420
QY 421 AGCATTGTTGCAACAAATATTAGTGGCGAAATTCGCAGTTCAAAATTTAATATGTGATG 480
Db 421 AGCATTGTTGCAACAAATATTAGTGGCGAAATTCGCAGTTCAAAATTTAATATGTGATG 480
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Db 481 GGTGTTGCTTAAAGCGAGCTTAGAACCAATGTTAAATATTAGCATTAGCTTAGTTCCT 540
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Db 541 GATAATATTTCGGCTTAATGCAATTTAGTGGCGAAATTCGCAGTTCAAAATTTAATATGTGATG 600
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QY 721 GTTACAGGTGAAAAATATTTCATGTAGATAGCGGATTCACGCAATTAATAA 771
Db 721 GTTACAGGTGAAAAATATTTCATGTAGATAGCGGATTCACGCAATTAATAA 771
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## RESULT 3

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US-10-138-701-5
; Sequence 5, Application US/10138701
; Patent No. 6753149
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc. et al.
; TITLE OF INVENTION: Staphylococcus aureus genes and polypeptides
; FILE REFERENCE: PB484
; CURRENT APPLICATION NUMBER: US/10/138,701
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: US/09/512,255A
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; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/098,964  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: US 60/009,861  
; PRIOR FILING DATE: 1996-01-05  
; PRIOR APPLICATION NUMBER: PCT/ US99/19726  
; PRIOR FILING DATE: 1999-08-31  
; PRIOR APPLICATION NUMBER: US 08/956,171  
; PRIOR FILING DATE: 1997-10-20  
; NUMBER OF SEQ ID NOS: 61  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 5  
; LENGTH: 916  
; TYPE: DNA  
; ORGANISM: Staphylococcus aureus  
US-10-138-701-5

Query Match 65.6%; Score 506; DB 4; Length 916;  
Best Local Similarity 99.5%; Pred. No. 2.5e-247;  
Matches 656; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ATGTTAAATCTTGAAACAAACAAACATATGTCATCATGGGAATCGCTAATAAGCGTAGTATT 60  
Db |||||||  
Qy 96 ATGTTAAATCTTGAAACAAACAAACATATGTCATCATGGGAATCGCTAATAAGCGTAGTATT 155  
Db |||||||  
Qy 61 GCTTTTGGTGCCTAAAGTTTGTAGATCAATTAGGTGCTAAATAGTATTACTTACCGT 120  
Db |||||||  
Qy 156 GCTTTTGGTGCCTAAAGTTTGTAGATCAATTAGGTGCTAAATAGTATTACTTACCGT 215  
Db |||||||  
Qy 121 AAGAACGTCGCGTAAGGCTTGGAATTAATTAAGCAATTAATCAACAGGCG 180  
Db |||||||  
Qy 216 AAGAACGTCGCGTAAGGCTTGGAATTAATTAAGCAATTAATCAACAGGCG 275  
Db |||||||  
Qy 181 CACTTATATCAAAATTCATGTTCAAGCGATGAAGGTTAATAGTTTGTAGCAAAAT 240  
Db |||||||  
Qy 276 CACTTATATCAAAATTCATGTTCAAGCGATGAAGGTTAATAGTTTGTAGCAAAAT 335  
Db |||||||  
Qy 241 GGTAAAGATGTTGGCAATATGATGTTATATATCAATTCGCAATTTGCTAATATGGAA 300  
Db |||||||  
Qy 336 GGTAAAGATGTTGGCAATATGATGTTATATATCAATTCGCAATTTGCTAATATGGAA 395  
Db |||||||  
Qy 301 GACTTAGCGGAGCTTTCTGAACTTCAGTGAAGGCTTCTGTTAGTCAAGCAAT 360  
Db |||||||  
Qy 396 GACTTAGCGGAGCTTTCTGAACTTCAGTGAAGGCTTCTGTTAGTCAAGCAAT 455  
Db |||||||  
Qy 361 AGTTCCTACTCATTAACAAATGTTGGCTCATGAAGCTAATAAATAATATGCCAGAGTGGT 420  
Db |||||||  
Qy 456 AGTTCCTACTCATTAACAAATGTTGGCTCATGAAGCTAATAAATAATATGCCAGAGTGGT 515  
Db |||||||  
Qy 421 AGCAATGTTGCAACACATATTTAGGTGGCAATTCGCAATTCAGAAATTAATATGATG 480  
Db |||||||  
Qy 516 AGCAATGTTGCAACACATATTTAGGTGGCAATTCGCAATTCAGAAATTAATATGATG 575  
Db |||||||  
Qy 481 GGTGTTGCTAAGCGAGCTTAGAAGCAATGTTAAATATTTAGCATTAGCATTAGTCTCT 540  
Db |||||||  
Qy 576 GGTGTTGCTAAGCGAGCTTTAGAAGCAATGTTAAATATTTAGCATTTAGCATTTAGTCCA 635  
Db |||||||  
Qy 541 GATAATATTCGCTTAATGCAATTCAGTGGTCCCAATCGTACATTTAAGTCAAAAGGT 600  
Db |||||||  
Qy 636 GATAATATTCGCTTAATGCAATTTAGTGGTCCCAATCGTACATTTAGTCAAAAGGT 695  
Db |||||||  
Qy 601 GTGGGTGTTTCAATCAAAATTTTAAAGAAATCGAAGAGCGTGCACCTTTTAAACGTAA 659  
Db |||||||  
Qy 696 GTGGGTGTTTCAATCAAAATTTTAAAGAAATCGAAGAGCGTGCACCTTTTAAACGTAA 754  
Db |||||||

## RESULT 4

US-08-956-171E-772  
; Sequence 772, Application US/08956171E  
; Patent No. 6593114  
; GENERAL INFORMATION:  
; APPLICANT: Charles Kunsch  
; Gil H. Choi

Patrick S. Dillon  
Craig A. Rosen  
Steven C. Barash  
Michael R. Fannon  
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences  
NUMBER OF SEQUENCES: 5256  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: Maryland  
COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
COMPUTER: HP Vectra 486/33  
OPERATING SYSTEM: MSDOS version 6.2  
SOFTWARE: ASCII Text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/956,171E  
FILING DATE: 20-Oct-1997  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/009,861  
FILING DATE: January 5, 1996  
APPLICATION NUMBER: 08/781,986  
FILING DATE: January 3, 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Mark J. Hyman  
REGISTRATION NUMBER: 46,789  
REFERENCE/DOCKET NUMBER: PB248P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (240) 314-1224  
TELEFAX: (301) 309-8439  
INFORMATION FOR SEQ ID NO: 772:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 704 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 772:  
US-08-956-171E-772

Query Match 56.7%; Score 437; DB 4; Length 704;  
Best Local Similarity 99.6%; Pred. No. 3.1e-212;  
Matches 537; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATGTTAAATCTTGAAACAAACAAACATATGTCATCATGGGAATCGCTAATAAGCGTAGTATT 60  
Db |||||||  
Qy 24 ATGTTAAATCTTGAAACAAACAAACATATGTCATCATGGGAATCGCTAATAAGCGTAGTATT 83  
Db |||||||  
Qy 61 GCTTTTGGTGCCTAAAGTTTGTAGATCAATTAGGTGCTAAAATTAGTATTACTTACCGT 120  
Db |||||||  
Qy 84 GCTTTTGGTGCCTAAAGTTTGTAGATCAATTAGGTGCTAAAATTAGTATTACTTACCGT 143  
Db |||||||  
Qy 121 AAGAACGTCGCGTAAGGCTTGGAATTAATTAAGCAATTAATCAACAGGCG 180  
Db |||||||  
Qy 144 AAGAACGTCGCGTAAGGCTTGGAATTAATTAAGCAATTAATCAACAGGCG 203  
Db |||||||  
Qy 181 CACTTATATCAAAATTCATGTTCAAGCGATGAAGGTTAATAGTTTGTAGCAAAAT 240  
Db |||||||  
Qy 204 CACTTATATCAAAATTCATGTTCAAGCGATGAAGGTTAATAGTTTGTAGCAAAAT 263  
Db |||||||  
Qy 241 GGTAAAGATGTTGGCAATATTCATGTTGATATCAATCGCATTTGCTAATATGGAA 300  
Db |||||||  
Qy 264 GGTAAAGATGTTGGCAATATTCATGTTGATATCAATCGCATTTGCTAATATGGAA 323  
Db |||||||  
Qy 301 GACTTAGCGGAGCTTTCTGAACTTCAGTGAAGGCTTCTGTTAGTCAAGCAAT 360  
Db |||||||  
Qy 324 GACTTAGCGGAGCTTTCTGAACTTCAGTGAAGGCTTCTGTTAGTCAAGCAAT 383  
Db |||||||  
Qy 361 AGTTCCTACTCATTAACAAATTCATGAGCTAATAAATAATAGTCCAGAGGCGT 420  
Db |||||||

Db 384 AGTTCTTACTATTAAACAATTGGCTCATGAAGCTAAAAAATTAAATGCCAGAAGTGT 443  
QY 421 AGCAATTTGGCAACAACATATTAGTGGCGAATTCGCGATTCCAAATATTAAATGTGATG 480  
Db 444 AGCAATTTGGCAACAACATATTAGTGGCGAATTCGCGATTCCAAATATTAAATGTGATG 503  
QY 481 GGTGTTGCTAAAGCGAGCTTAGAAGCAAAATGTTAAATATTAGCATTTAGCTTACGTC 539  
Db 504 GGTGTTGCTAAAGCGAGCTTAGAAGCAAAATGTTAAATATTAGCATTTAGCTTACGTC 562

RESULT 5  
US-08-781-986A-772  
; Sequence 772, Application US/08781986A  
; Patent No. 6737248  
; GENERAL INFORMATION:  
; APPLICANT: Charles Kunsch  
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences  
; NUMBER OF SEQUENCES: 5255  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Human Genome Sciences, Inc.  
; STREET: 9410 Key West Avenue  
; CITY: Rockville  
; STATE: Maryland  
; COUNTRY: USA  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
; COMPUTER: HP Vectra 486/33  
; OPERATING SYSTEM: MSDOS version 6.2  
; SOFTWARE: ASCII Text  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/781,986A  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Benson, Bob  
; REGISTRATION NUMBER: 30,446  
; REFERENCE/DOCKET NUMBER: PB248PP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (301) 309-8504  
; TELEFAX: (301) 309-8512 772:  
; INFORMATION FOR SEQ ID NO: 772:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 704 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; US-08-781-986A-772

Query Match 56.7%; Score 437; DB 4; Length 704;  
Best Local Similarity 99.6%; Pred. No. 3.1e-212;  
Matches 537; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGTTAAATCTTGAAACAAAACATATGTCATCATCGGAATCGCTAAATGAAGCGTAGTATT 60  
Db 24 ATGTTAAATCTTGAAACAAAACATATGTCATCATCGGAATCGCTAAATGAAGCGTAGTATT 83  
QY 61 GCTTTTGGTGCCTAAAGCTTTTAGTCAATTAGTGTCAATTAATAGTATTACTTTACCGT 120  
Db 84 GCTTTTGGTGCCTAAAGCTTTTAGTCAATTAGTGTCAATTAATAGTATTACTTTACCGT 143  
QY 121 AAAGACGTAGCGGTAAAGAGCTTGAAAAATATTAGAAACAATTAATCAACAGAGCG 180  
Db 144 AAAGACGTAGCGGTAAAGAGCTTGAAAAATATTAGAAACAATTAATCAACAGAGCG 203  
QY 181 CACTTATATCAATTTGATGTTCAAGCGGATGAAGAGTTATTAAATGGTTTTCAGCAAAATT 240  
Db 204 CACTTATATCAATTTGATGTTCAAGCGGATGAAGAGTTATTAAATGGTTTTCAGCAAAATT 263

QY 241 GGTAAAGATGTTGGCAATATTGATGGTGTATATATCATTAATCGCATTTTGTCTAATATGAA 300  
Db 264 GGTAAAGATGTTGGCAATATTGATGGTGTATATATCATTAATCGCATTTTGTCTAATATGAA 323  
QY 301 GACTTTACGCGGACGCTTTTCTGAAACTTTCACGTGAAGGCTTCTTGTAGCTCAAGACATT 360  
Db 324 GACTTTACGCGGACGCTTTTCTGAAACTTTCACGTGAAGGCTTCTTGTAGCTCAAGACATT 383  
QY 361 AGTTCTTACTATTAACAATTTGTGGCTCATGAAGCTAAAAAATTAATGCCAGAAGTGT 420  
Db 384 AGTTCTTACTATTAAACAATTTGTGGCTCATGAAGCTAAAAAATTAATGCCAGAAGTGT 443  
QY 421 AGCAATTTGGCAACAACATATTAGTGGCGAATTCGCGATTCCAAATATTAAATGTGATG 480  
Db 444 AGCAATTTGGCAACAACATATTAGTGGCGAATTCGCGATTCCAAATATTAAATGTGATG 503  
QY 481 GGTGTTGCTAAAGCGAGCTTAGAAGCAAAATGTTAAATATTAGCATTTAGCTTACGTC 539  
Db 504 GGTGTTGCTAAAGCGAGCTTAGAAGCAAAATGTTAAATATTAGCATTTAGCTTACGTC 562

RESULT 6  
US-08-956-171E-514/c  
; Sequence 514, Application US/08956171E  
; Patent No. 6593114  
; GENERAL INFORMATION:  
; APPLICANT: Charles Kunsch  
; Gil H. Choi  
; Patrick S. Dillon  
; Craig A. Rosen  
; Steven C. Barash  
; Michael R. Fannon  
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences  
; NUMBER OF SEQUENCES: 5256  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Human Genome Sciences, Inc.  
; STREET: 9410 Key West Avenue  
; CITY: Rockville  
; STATE: Maryland  
; COUNTRY: USA  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
; COMPUTER: HP Vectra 486/33  
; OPERATING SYSTEM: MSDOS version 6.2  
; SOFTWARE: ASCII Text  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/956,171E  
; FILING DATE: 20-Oct-1997  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/009,861  
; FILING DATE: January 5, 1996  
; APPLICATION NUMBER: 08/781,986  
; FILING DATE: January 3, 1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mark J. Hyman  
; REGISTRATION NUMBER: 46,789  
; REFERENCE/DOCKET NUMBER: PB248P1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (240) 314-1224  
; TELEFAX: (301) 309-8439  
; INFORMATION FOR SEQ ID NO: 514:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 587 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 514:  
; US-08-956-171E-514

Query Match 8.2%; Score 63; DB 4; Length 587;  
Best Local Similarity 100.0%; Pred. No. 5.5e-22;

Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 709 TTATCAAGTGGCGTTACAGGTGAAATATTTCATGTAGATAGCGGATTCACGCAATTAAA 768  
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Db 547 TTATCAAGTGGCGTTACAGGTGAAATATTTCATGTAGATAGCGGATTCACGCAATTAAA 488

QY 769 TAA 771

Db 487 TAA 485

## RESULT 7

US-08-781-986A-514/c  
; Sequence 514, Application US/08781986A  
; Patent No. 6737248  
; GENERAL INFORMATION:  
; APPLICANT: Charles Kunsch  
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences  
; NUMBER OF SEQUENCES: 5255  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Human Genome Sciences, Inc.  
; STREET: 9410 Key West Avenue  
; CITY: Rockville  
; STATE: Maryland  
; COUNTRY: USA  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
; COMPUTER: HP Vectra 486/33  
; OPERATING SYSTEM: MSDOS version 6.2  
; SOFTWARE: ASCII Text  
; APPLICATION DATA:  
; APPLICATION NUMBER: US/08/781,986A  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Benson, Bob  
; REGISTRATION NUMBER: 30,446  
; REFERENCE/DOCKET NUMBER: PB248PP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (301) 309-8504  
; TELEFAX: (301) 309-8512  
; INFORMATION FOR SEQ ID NO: 514:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 587 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear

US-08-781-986A-514

Query Match 8.2%; Score 63; DB 4; Length 587;  
Best Local Similarity 100.0%; Pred. No. 5.5e-22;  
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 709 TTATCAAGTGGCGTTACAGGTGAAATATTTCATGTAGATAGCGGATTCACGCAATTAAA 768  
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Db 547 TTATCAAGTGGCGTTACAGGTGAAATATTTCATGTAGATAGCGGATTCACGCAATTAAA 488  
QY 769 TAA 771  
Db 487 TAA 485

## RESULT 8

US-10-089-740-1  
; Sequence 1, Application US/10089740  
; Patent No. 6730684  
; GENERAL INFORMATION:  
; APPLICANT: Miller, William H.  
; APPLICANT: Newlander, Kenneth A.

; APPLICANT: Seefeld, Mark A.  
; APPLICANT: Uzinskas, Irene N.  
; TITLE OF INVENTION: Fab I Inhibitors  
; FILE REFERENCE: P51038  
; CURRENT APPLICATION NUMBER: US/10/089,740  
; CURRENT FILING DATE: 2000-10-10  
; PRIOR APPLICATION NUMBER: 60/158,707  
; PRIOR FILING DATE: 1999-10-08  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 39  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-089-740-1

Query Match 3.9%; Score 30; DB 4; Length 39;  
Best Local Similarity 100.0%; Pred. No. 3.4e-05;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTTAAATCTTGAACAAACAAACATATGTC 30  
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Db 10 ATGTTAAATCTTGAACAAACAAACATATGTC 39

## RESULT 9

US-09-292-411A-3  
; Sequence 3, Application US/09292411A  
; Patent No. 6753172  
; GENERAL INFORMATION:  
; APPLICANT: Lonsdale, John  
; APPLICANT: Milner, Peter  
; APPLICANT: Payne, David  
; APPLICANT: Pearson, Stewart  
; TITLE OF INVENTION: FABI  
; FILE REFERENCE: GMS0005-D1  
; CURRENT APPLICATION NUMBER: US/09/292,411A  
; CURRENT FILING DATE: 1999-04-15  
; PRIOR APPLICATION NUMBER: US 08/790,043  
; PRIOR FILING DATE: 1997-01-28  
; PRIOR APPLICATION NUMBER: US 60/024,845  
; PRIOR FILING DATE: 1996-08-26  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 39  
; TYPE: DNA  
; ORGANISM: Staphylococcus aureus  
US-09-292-411A-3

Query Match 3.9%; Score 30; DB 4; Length 39;  
Best Local Similarity 100.0%; Pred. No. 3.4e-05;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTTAAATCTTGAACAAACAAACATATGTC 30  
|||||  
Db 10 ATGTTAAATCTTGAACAAACAAACATATGTC 39

## RESULT 10

US-10-089-739-1  
; Sequence 1, Application US/10089739  
; Patent No. 6762201  
; GENERAL INFORMATION:  
; APPLICANT: Miller, William H.  
; APPLICANT: Newlander, Kenneth A.  
; APPLICANT: Seefeld, Mark A.  
; TITLE OF INVENTION: Fab I Inhibitors  
; FILE REFERENCE: P51037  
; CURRENT APPLICATION NUMBER: US/10/089,739  
; CURRENT FILING DATE: 2002-08-20  
; PRIOR APPLICATION NUMBER: 60/158,529  
; PRIOR FILING DATE: 1999-10-08

; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 39  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-089-739-1

Query Match 3.9%; Score 30; DB 4; Length 39;  
Best Local Similarity 100.0%; Pred. No. 3.4e-05;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 10 ATGTTAAATCTTGAACAAACAAACATATGTC 39  
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RESULT 11  
US-09-134-001C-1172  
; Sequence 1172, Application US/09134001C  
; Patent No. 6380370  
; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS  
; FILE REFERENCE: GTC-007  
; CURRENT APPLICATION NUMBER: US/09/134,001C  
; CURRENT FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: US 60/064,964  
; PRIOR FILING DATE: 1997-11-08  
; PRIOR APPLICATION NUMBER: US 60/055,779  
; PRIOR FILING DATE: 1997-08-14  
; NUMBER OF SEQ ID NOS: 5674  
; SEQ ID NO 1172  
; LENGTH: 783  
; TYPE: DNA  
; ORGANISM: Staphylococcus epidermidis  
US-09-134-001C-1172

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Best Local Similarity 100.0%; Pred. No. 0.038;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 160 AAATTATTAGAACAAATTAATCAA 183  
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RESULT 12  
US-10-089-740-4/c  
; Sequence 4, Application US/10089740  
; Patent No. 6730684  
; GENERAL INFORMATION:  
; APPLICANT: Miller, William H.  
; APPLICANT: Newlander, Kenneth A.  
; APPLICANT: Seefeld, Mark A.  
; APPLICANT: Uzinskas, Irene N.  
; TITLE OF INVENTION: Fab I Inhibitors  
; FILE REFERENCE: P51038  
; CURRENT APPLICATION NUMBER: US/10/089,740  
; CURRENT FILING DATE: 2000-10-10  
; PRIOR APPLICATION NUMBER: 60/158,707  
; PRIOR FILING DATE: 1999-10-08  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 26  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-089-740-4

Query Match 3.0%; Score 23; DB 4; Length 26;  
Best Local Similarity 100.0%; Pred. No. 0.13;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 23 TTAATCTTGAACAAACAAACATA 1  
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RESULT 13  
US-10-089-739-4/c  
; Sequence 4, Application US/10089739  
; Patent No. 6762201  
; GENERAL INFORMATION:  
; APPLICANT: Miller, William H.  
; APPLICANT: Newlander, Kenneth A.  
; APPLICANT: Seefeld, Mark A.  
; TITLE OF INVENTION: Fab I Inhibitors  
; FILE REFERENCE: P51037  
; CURRENT APPLICATION NUMBER: US/10/089,739  
; CURRENT FILING DATE: 2002-08-20  
; PRIOR APPLICATION NUMBER: 60/158,529  
; PRIOR FILING DATE: 1999-10-08  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 26  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-089-739-4

Query Match 3.0%; Score 23; DB 4; Length 26;  
Best Local Similarity 100.0%; Pred. No. 0.13;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTAATCTTGAACAAACAAACATA 26  
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Db 23 TTAATCTTGAACAAACAAACATA 1  
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RESULT 14  
US-10-089-740-3  
; Sequence 3, Application US/10089740  
; Patent No. 6730684  
; GENERAL INFORMATION:  
; APPLICANT: Miller, William H.  
; APPLICANT: Newlander, Kenneth A.  
; APPLICANT: Seefeld, Mark A.  
; APPLICANT: Uzinskas, Irene N.  
; TITLE OF INVENTION: Fab I Inhibitors  
; FILE REFERENCE: P51038  
; CURRENT APPLICATION NUMBER: US/10/089,740  
; CURRENT FILING DATE: 2000-10-10  
; PRIOR APPLICATION NUMBER: 60/158,707  
; PRIOR FILING DATE: 1999-10-08  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 28  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-089-740-3

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Best Local Similarity 100.0%; Pred. No. 1.3;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 8 TTAATCTTGAACAAACAAACATA 28  
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RESULT 15  
US-10-089-739-3  
; Sequence 3, Application US/10089739

; Patent No. 6762201  
; GENERAL INFORMATION:  
; APPLICANT: Miller, William H.  
; APPLICANT: Newlander, Kenneth A.  
; APPLICANT: Seefeld, Mark A.  
; TITLE OF INVENTION: Fab I Inhibitors  
; FILE REFERENCE: P51037  
; CURRENT APPLICATION NUMBER: US/10/089,739  
; CURRENT FILING DATE: 2002-08-20  
; PRIOR APPLICATION NUMBER: 60/158,529  
; PRIOR FILING DATE: 1999-10-08  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 28  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-089-739-3

Query Match 2.7%; Score 21; DB 4; Length 28;  
Best Local Similarity 100.0%; Pred. No. 1.3;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 8 TTAATCTTGAACAAAAACA 28  
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

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(without alignments)  
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Perfect score: 771  
Sequence: 1 ATGTTAAATCTTGAAACAA.....GATTCACGCAGTAATAATAA 771

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Gapop 60.0 , Gapext 60.0

Searched: 733684 seqs, 3274456166 residues

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Minimum DB seq length: 0  
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14: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:\*  
15: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*  
16: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq:\*  
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19: /cgn2\_6/ptodata/1/pubpna/US10G\_PUBCOMB.seq:\*  
20: /cgn2\_6/ptodata/1/pubpna/US10H\_PUBCOMB.seq:\*  
21: /cgn2\_6/ptodata/1/pubpna/US10I\_PUBCOMB.seq:\*  
22: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*  
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26: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	771	100.0	771	21	US-10-888-524-1
2	720	93.4	771	17	US-10-282-122A-7734
3	720	93.4	771	21	US-10-857-625-263
4	720	93.4	6985	21	US-10-857-625-34
5	557	72.2	771	9	US-09-815-242-8794
6	506	65.6	916	16	US-10-138-701-5
7	506	65.6	916	20	US-10-823-785-5
					Sequence 1, Appli
					Sequence 7734, Ap
					Sequence 263, App
					Sequence 34, Appl
					Sequence 8794, Ap
					Sequence 5, Appli
					Sequence 5, Appli

ALIGNMENTS

RESULT 1  
US-10-888-524-1  
; Sequence 1, Application US/10888524  
; Publication No. US20050112713A1  
; GENERAL INFORMATION:  
; APPLICANT: DEWOLF JR., WALTER E.  
; APPLICANT: PAYNE, DAVID JOHN  
; APPLICANT: MILNER, PETER HENRY  
; APPLICANT: PEARSON, STEWART CAMPBELL  
; APPLICANT: LONSDALE, JOHN TIMOTHY  
; TITLE OF INVENTION: METHODS OF USING FAB I AND COMPOUNDS MODULATING FAB I ACTIVITY  
; FILE REFERENCE: IPT-061.02  
; CURRENT APPLICATION NUMBER: US/10/888,524  
; CURRENT FILING DATE: 2004-07-09  
; PRIOR APPLICATION NUMBER: 60/024,845  
; PRIOR FILING DATE: 1996-08-28  
; PRIOR APPLICATION NUMBER: 08/790,043  
; PRIOR FILING DATE: 1997-08-28  
; PRIOR APPLICATION NUMBER: 60/134,362  
; PRIOR FILING DATE: 1999-05-14  
; PRIOR APPLICATION NUMBER: 10/009,219  
; PRIOR FILING DATE: 2001-11-07  
; PRIOR APPLICATION NUMBER: PCT/US00/12104  
; PRIOR FILING DATE: 2000-05-04  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn Ver. 3.3  
; SEQ ID NO 1  
; LENGTH: 771  
; TYPE: DNA  
; ORGANISM: Staphylococcus aureus

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Sequence 1963, Ap  
Sequence 4490, Ap  
Sequence 4491, Ap  
Sequence 772, App  
Sequence 772, App  
Sequence 1697, Ap  
Sequence 3050, Ap  
Sequence 4234, Ap  
Sequence 5569, Ap  
Sequence 1666, Ap  
Sequence 4233, Ap  
Sequence 4173, Ap  
Sequence 8437, Ap  
Sequence 2214, Ap  
Sequence 2218, Ap  
Sequence 2219, Ap  
Sequence 2529, Ap  
Sequence 3421, Ap  
Sequence 4728, Ap  
Sequence 4739, Ap  
Sequence 4747, Ap  
Sequence 5075, Ap  
Sequence 5076, Ap  
Sequence 3021, Ap  
Sequence 5575, Ap  
Sequence 514, App  
Sequence 514, App  
Sequence 2921, Ap  
Sequence 5478, Ap  
Sequence 3, Appli  
Sequence 3455, A  
Sequence 2044, Ap  
Sequence 24707, A  
Sequence 41051, A  
Sequence 144, App  
Sequence 6, Appli  
Sequence 78598, A

US-10-888-524-1

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 771; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 ATGTTAAATCTTGAAACAAACATATGTCATCGGAATCGCTAATAAGCGTAGTATT 60

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DB 61 GCTTTTGGTGCCTAAAGTTTTAGATCAATTAGGTGCTGCTAATAAGTTACTTACCGT 120

QY 121 AAAGAACGTAGCGCTTAAGAGCTTGAAATTTATTAGAACATTAATCAACAGAGCG 180
DB 121 AAAGAACGTAGCGCTTAAGAGCTTGAAATTTATTAGAACATTAATCAACAGAGCG 180

QY 181 CACTTATATCAAAATGATGTTCAAGCGATGAAGAGTTATTAAATGGTTTTGAGCAAAATT 240
DB 181 CACTTATATCAAAATGATGTTCAAGCGATGAAGAGTTATTAAATGGTTTTGAGCAAAATT 240

QY 241 GGTAAAGATGTTGGCAATATTGATGGTGPATATCAATCGCAATTTGCTAATATGAA 300
DB 241 GGTAAAGATGTTGGCAATATTGATGGTGPATATCAATCGCAATTTGCTAATATGAA 300

QY 301 GACTTACGGGAGCGCTTTCTGAAACTTCACGTGAAGGCTTCTTGTAGCTCAAGACATT 360
DB 301 GACTTACGGGAGCGCTTTCTGAAACTTCACGTGAAGGCTTCTTGTAGCTCAAGACATT 360

QY 361 AGTTCTTACTCAATTAACAAATGCTCATGAAGCTTAAATAATTAATGCGAAGGTGGT 420
DB 361 AGTTCTTACTCAATTAACAAATGCTCATGAAGCTTAAATAATTAATGCGAAGGTGGT 420

QY 421 AGCATTTGTCACAAACATATTTAGGTGGCGCAATTCGCAGTTCAAAAATTTAATGTGATG 480
DB 421 AGCATTTGTCACAAACATATTTAGGTGGCGCAATTCGCAGTTCAAAAATTTAATGTGATG 480

QY 481 GGTGATCAAGTGAAGTAGGTAAAGCAATTTAGTGGCGAATTCGCGAATTTAATAATGTGATG 480
DB 481 GGTGATCAAGTGAAGTAGGTAAAGCAATTTAGTGGCGAATTCGCGAATTTAATAATGTGATG 480

QY 541 GATAATATTCGCGTTAATGCAATTTTCAATCGCTGCTCAATCGTACATTAAGTGCAGAAAGT 600
DB 541 GATAATATTCGCGTTAATGCAATTTTCAATCGCTGCTCAATCGTACATTAAGTGCAGAAAGT 600

QY 601 GTGGGTGGTTTTCAATACAAATCTTAAAGAAATCGAAGAGCGTGCACCTTTAAACGTAAC 660
DB 601 GTGGGTGGTTTTCAATACAAATCTTAAAGAAATCGAAGAGCGTGCACCTTTAAACGTAAC 660

QY 661 GTTGATCAAGTGAAGTAGGTAAACAGCGGCTTACTTTRTAAAGTCACTTATCAAGTGGC 720
DB 661 GTTGATCAAGTGAAGTAGGTAAACAGCGGCTTACTTTRTAAAGTCACTTATCAAGTGGC 720

QY 721 GTTACAGGTGAAGTAAATATTCATGTAGATAGCGGATTCACGCAATTTAAATAA 771
DB 721 GTTACAGGTGAAGTAAATATTCATGTAGATAGCGGATTCACGCAATTTAAATAA 771
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RESULT 2

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US-10-282-122A-7734
; Sequence 7734, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangou
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
```

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; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7734
; LENGTH: 771
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-282-122A-7734
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Query Match      93.4%; Score 720; DB 17; Length 771;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 770; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGTTAAATCTTGAAACAAACATATGTCATCGGAATCGCTAATAAGCGTAGTATT 60
DB 1 ATGTTAAATCTTGAAACAAACATATGTCATCGGAATCGCTAATAAGCGTAGTATT 60

QY 61 GCTTTTGGTGCCTAAAGTTTTAGATCAATTAGGTGCTAATAAGTTACTTACCGT 120
DB 61 GCTTTTGGTGCCTAAAGTTTTAGATCAATTAGGTGCTAATAAGTTACTTACCGT 120

QY 121 AAAGAACGTAGCGCTTAAGAGCTTGAAATTTATTAGAACATTAATCAACAGAGCG 180
DB 121 AAAGAACGTAGCGCTTAAGAGCTTGAAATTTATTAGAACATTAATCAACAGAGCG 180

QY 181 CACTTATATCAAAATGATGTTCAAGCGATGAAGAGTTATTAAATGGTTTTGAGCAAAATT 240
DB 181 CACTTATATCAAAATGATGTTCAAGCGATGAAGAGTTATTAAATGGTTTTGAGCAAAATT 240

QY 241 GGTAAAGATGTTGGCAATATTGATGGTGPATATCAATCGCAATTTGCTAATATGAA 300
DB 241 GGTAAAGATGTTGGCAATATTGATGGTGPATATCAATCGCAATTTGCTAATATGAA 300

QY 301 GACTTACGGGAGCGCTTTCTGAAACTTCACGTGAAGGCTTCTTGTAGCTCAAGACATT 360
DB 301 GACTTACGGGAGCGCTTTCTGAAACTTCACGTGAAGGCTTCTTGTAGCTCAAGACATT 360

QY 361 AGTTCTTACTCAATTAACAAATTTAGGTGGCTCATGAAGCTAATAAATTAATGCCAGAGGTGGT 420
DB 361 AGTTCTTACTCAATTAACAAATTTAGGTGGCTCATGAAGCTAATAAATTAATGCCAGAGGTGGT 420

QY 421 AGCATTTGTCACAAACATATTTAGGTGGCGCAATTCGCAGTTCAAAAATTTAATGTGATG 480
DB 421 AGCATTTGTCACAAACATATTTAGGTGGCGCAATTCGCAGTTCAAAAATTTAATGTGATG 480

QY 481 GGTGATCAAGTGAAGTAGGTAAAGCAATTTAGTGGCGAATTCGCGAATTTAATAATGTGATG 540
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Db 481 |GGTGTCTCTAAGCGAGCTTAGAAGCAAAATGTTAAATATTTAGCATTTAGAGTCTT 540
Qy 541 |GATAAATATTCGCGTTAATGCAAAATTCAGCTGGTCCAAATCCGTACATTTAAGTGCAAAAGGT 600
Db 541 |GATAAATATTCGCGTTAATGCAAAATTCAGCTGGTCCAAATCCGTACATTTAAGTGCAAAAGGT 600
Qy 601 |GTGGGTGGTTTCAATACAATTCCTTAAAGAAATCGAAGAGCGTGCACTTTTAAACGTAAC 660
Db 601 |GTGGGTGGTTTCAATACAATTCCTTAAAGAAATCGAAGAGCGTGCACTTTTAAACGTAAC 660
Qy 661 |GTTGATCAAGTAGAAGTAGTAAACAGCGCTTACTTCTTAAAGTGAAGTATCAAGTGGC 720
Db 661 |GTTGATCAAGTAGAAGTAGTAAACAGCGCTTACTTCTTAAAGTGAAGTATCAAGTGGC 720
Qy 721 |GTTACAGGTGAAAATATTCATGTAGATAGCGGAATCCACGCAATTTAAATAA 771
Db 721 |GTTACAGGTGAAAATATTCATGTAGATAGCGGAATCCACGCAATTTAAATAA 771

RESULT 3
US-10-857-625-263
; Sequence 263, Application US/10857625
; Publication No. US20050026189A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; TITLE OF INVENTION: MICROBIAL OPERONS
; FILE REFERENCE: ELITRA.036A
; CURRENT APPLICATION NUMBER: US/10/857,625
; CURRENT FILING DATE: 2004-05-28
; PRIOR FILING DATE: 2003-05-29
; NUMBER OF SEQ ID NOS: 833
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 263
; LENGTH: 771
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-857-625-263

Query Match 93.4%; Score 720; DB 21; Length 771;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 770; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGTTAAATCTTGAACAAACAAACATATGTCATCGGAATCGCTAATAGCGTAGTATT 60
Db 1 ATGTTAAATCTTGAACAAACAAACATATGTCATCGGAATCGCTAATAGCGTAGTATT 60
Qy 61 GCTTTTGGTGTGCTAAAGTTTGTAGATCAATTAGGTGCTAAATTAGTATTACTTACCGT 120
Db 61 GCTTTTGGTGTGCTAAAGTTTGTAGATCAATTAGGTGCTAAATTAGTATTACTTACCGT 120
Qy 121 AAAGACGTAGCGCTAAAGAGCTTGAAAATTTATAGAACAAATTAATCAACAGAGCG 180
Db 121 AAAGACGTAGCGCTAAAGAGCTTGAAAATTTATAGAACAAATTAATCAACAGAGCG 180
Qy 181 CACTTATATCAAAATTTGATGTTCAAAGCGATGAAGAGGTATTAAATGTTTGAAGCAAAATT 240
Db 181 CACTTATATCAAAATTTGATGTTCAAAGCGATGAAGAGGTATTAAATGTTTGAAGCAAAATT 240
Qy 241 GGTAAAGATGTTGGCAATATTTGATGTTGATATCATTTCAATCGCATTTGCTAATATGGAA 300
Db 241 GGTAAAGATGTTGGCAATATTTGATGTTGATATCATTTCAATCGCATTTGCTAATATGGAA 300
Qy 301 GACTTACGCGGAGCGCTTTCTGAAAATTCACGTGAAGGCTTCTTGTAGCTCAAGACATT 360
Db 301 GACTTACGCGGAGCGCTTTCTGAAAATTCACGTGAAGGCTTCTTGTAGCTCAAGACATT 360
Qy 361 AGTTCTTACTTAAACAAATTTGGCTCATGAGCTTAAACAAATTAATGCCAGAGGTGGT 420
Db 361 AGTTCTTACTTAAACAAATTTGGCTCATGAGCTTAAACAAATTAATGCCAGAGGTGGT 420
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Qy 421 AGCAATGTTGCAACAAACATATTTAGGTGGCAATTCGCAGTTCCAAAATTTAATATGTGATG 480
Db 421 AGCAATGTTGCAACAAACATATTTAGGTGGCAATTCGCAGTTCCAAAATTTAATATGTGATG 480
Qy 481 GGTGTTGCTTAAAGCGAGCTTTAGAAGCAAAATGTTAAATATTTAGCATTTAGACTTAGGTCTCT 540
Db 481 GGTGTTGCTTAAAGCGAGCTTTAGAAGCAAAATGTTAAATATTTAGCATTTAGACTTAGGTCTCT 540
Qy 541 GATAATATTTCCGGTTAATGCAAAATTTCCAGCTGGTCCAAATCCGTACATTTAAGTGCAAAAGGT 600
Db 541 GATAATATTTCCGGTTAATGCAAAATTTCCAGCTGGTCCAAATCCGTACATTTAAGTGCAAAAGGT 600
Qy 601 GTGGGTGGTTTCAATCAAAATTCCTTAAAGAAATCGAAGAGCGTGCACTTTTAAACGTAAC 660
Db 601 GTGGGTGGTTTCAATCAAAATTCCTTAAAGAAATCGAAGAGCGTGCACTTTTAAACGTAAC 660
Qy 661 GTTGATCAAGTAGAAGTAGTAAACAGCGCTTACTTCTTAAAGTGAAGTATCAAGTGGC 720
Db 661 GTTGATCAAGTAGAAGTAGTAAACAGCGCTTACTTCTTAAAGTGAAGTATCAAGTGGC 720
Qy 721 GTTACAGGTGAAAATATTCATGTAGATAGCGGAATCCACGCAATTTAAATAA 771
Db 721 GTTACAGGTGAAAATATTCATGTAGATAGCGGAATCCACGCAATTTAAATAA 771

RESULT 4
US-10-857-625-34
; Sequence 34, Application US/10857625
; Publication No. US20050026189A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; TITLE OF INVENTION: MICROBIAL OPERONS
; FILE REFERENCE: ELITRA.036A
; CURRENT APPLICATION NUMBER: US/10/857,625
; CURRENT FILING DATE: 2004-05-28
; PRIOR FILING DATE: 2003-05-29
; NUMBER OF SEQ ID NOS: 833
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34
; LENGTH: 6985
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-857-625-34

Query Match 93.4%; Score 720; DB 21; Length 6985;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 770; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGTTAAATCTTGAACAAACAAACATATGTCATCGGAATCGCTAATAGCGTAGTATT 60
Db 6215 ATGTTAAATCTTGAACAAACAAACATATGTCATCGGAATCGCTAATAGCGTAGTATT 6274
Qy 61 GCTTTTGGTGTGCTAAAGTTTGTAGATCAATTAGGTGCTAAATTAGTATTACTTACCGT 120
Db 6275 GCTTTTGGTGTGCTAAAGTTTGTAGATCAATTAGGTGCTAAATTAGTATTACTTACCGT 6334
Qy 121 AAAGACGTAGCGCTAAAGAGCTTGAAAATTTATAGAACAAATTAATCAACAGAGCG 180
Db 6335 AAAGACGTAGCGCTAAAGAGCTTGAAAATTTATAGAACAAATTAATCAACAGAGCG 6394
Qy 181 CACTTATATCAAAATTTGATGTTCAAAGCGATGAAGAGGTATTAAATGTTTGAAGCAAAATT 240
Db 6395 CACTTATATCAAAATTTGATGTTCAAAGCGATGAAGAGGTATTAAATGTTTGAAGCAAAATT 6454
Qy 241 GGTAAAGATGTTGGCAATATTTGATGTTGATATCATTTCAATCGCATTTGCTAATATGGAA 300
Db 6455 GGTAAAGATGTTGGCAATATTTGATGTTGATATCATTTCAATCGCATTTGCTAATATGGAA 6514
Qy 301 GACTTACGCGGAGCGCTTTCTGAAAATTCACGTGAAGGCTTCTTGTAGCTCAAGACATT 360
Db 6515 GACTTACGCGGAGCGCTTTCTGAAAATTCACGTGAAGGCTTCTTGTAGCTCAAGACATT 6574
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QY 361 AGTTCTTACTCATTAACAATTGTGGCTCATGAAGCTAAAAAATTAATGCCAGAGTGGT 420  
Db |||||||  
6575 AGTTCTTACTCATTAACAATTGTGGCTCATGAAGCTAAAAAATTAATGCCAGAGTGGT 6634  
QY 421 AGCATTGTTGCAACAACATATTTAGTGGCGCAATTCGCAGTTTCAAAATTTATAATGTGATG 480  
Db |||||||  
6635 AGCATTGTTGCAACAACATATTTAGTGGCGCAATTCGCAGTTTCAAAATTTATAATGTGATG 6694  
QY 481 GGTGTTGCTTAAAGCGAGCTTAGAAGCAAAATGTTAAATATTTAGCATTAGACTTAGTCTCT 540  
Db |||||||  
6695 GGTGTTGCTTAAAGCGAGCTTAGAAGCAAAATGTTAAATATTTAGCATTAGACTTAGTCTCT 6754  
QY 541 GATAATATTCGGGTTAATCAATTTTCAGCTGGTCCCAATCCGTACATTAAAGTGCAAAAAGGT 600  
Db |||||||  
6755 GATAATATTCGGGTTAATCAATTTTCAGCTGGTCCCAATCCGTACATTAAAGTGCAAAAAGGT 6814  
QY 601 GTGGGTGGTTCCTCAATACAATTTCTTAAAGAAATCGAAGAGCGTGCACCTTTAAAAAGCTAAC 660  
Db |||||||  
6815 GTGGGTGGTTCCTCAATACAATTTCTTAAAGAAATCGAAGAGCGTGCACCTTTAAAAAGCTAAC 6874  
QY 661 GTTGATCAAGTAGAAGTAGGTAAACAGCGGCTTACTTCTTAAAGTGAATTAATCAAGTGGC 720  
Db |||||||  
6875 GTTGATCAAGTAGAAGTAGGTAAACAGCGGCTTACTTCTTAAAGTGAATTAATCAAGTGGC 6934  
QY 721 GTTACAGGTGAAATATTCATGTAGATAGCGGATTCACGCAATTAATAAA 771  
Db |||||||  
6935 GTTACAGGTGAAATATTCATGTAGATAGCGGATTCACGCAATTAATAAA 6985

RESULT 5

US-09-815-242-8794  
; Sequence 8794, Application US/09815242  
; Patent No. US20020061569A1  
; GENERAL INFORMATION:  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Karl L.  
; APPLICANT: Zyskind, Judith W.  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John D.  
; APPLICANT: Carr, Grant J.  
; APPLICANT: Yamamoto, Robert T.  
; APPLICANT: Xu, H. Howard  
; TITLE OF INVENTION: Identification of Essential Genes in  
; TITLE OF INVENTION: Prokaryotes  
; FILE REFERENCE: ELITRA.011A  
; CURRENT APPLICATION NUMBER: US/09/815,242  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; NUMBER OF SEQ ID NOS: 1410  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8794  
; LENGTH: 771  
; TYPE: DNA  
; ORGANISM: Staphylococcus aureus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(771)  
US-09-815-242-8794

Query Match 72.2%; Score 557; DB 9; Length 771;  
Best Local Similarity 99.7%; Pred. No. 1.3e-268;  
Matches 557; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 ATGTTAAATCTTTGAAAAAACAACATATGTCATCATGCGAAATCGCTTAATAAGCGTAGTATT 60  
Db |||||||  
1 ATGTTAAATCTTTGAAAAAACAACATATGTCATCATGCGAAATCGCTTAATAAGCGTAGTATT 60  
QY 61 GCTTTTGTGTCGCTTAAAGATTTTAGATCAATTAGTGCTTAAATAGTATTTACTTTACCGT 120  
Db |||||||  
61 GCTTTTGTGTCGCTTAAAGATTTTAGATCAATTAGTGCTTAAATAGTATTTACTTTACCGT 120  
QY 121 AAAGAACGTAGCCGTAAAGAGCTTGAAAAATTTATTAGAACCAATTAATAACAACGAGCG 180  
Db |||||||  
121 AAAGAACGTAGCCGTAAAGAGCTTGAAAAATTTATTAGAACCAATTAATAACAACGAGCG 180  
QY 181 CACTTATATCAAAATGATGTTCAAAGCGATGAAGAGGTATTAAATGTTTGGTGGTGGTGGT 240  
Db |||||||  
181 CACTTATATCAAAATGATGTTCAAAGCGATGAAGAGGTATTAAATGTTTGGTGGTGGTGGT 240  
QY 241 GGTAAAGATGTTGGCAATATTGATGGTGTATATCAATTCGCAATTTGCTAAATATGGAA 300  
Db |||||||  
241 GGTAAAGATGTTGGCAATATTGATGGTGTATATCAATTCGCAATTTGCTAAATATGGAA 300  
QY 301 GACTTACGCGGACGCTTTTCTGAAACCTTCAGCTGAAGGCTTCTTCTTAGCTCAAGACATT 360  
Db |||||||  
301 GACTTACGCGGACGCTTTTCTGAAACCTTCAGCTGAAGGCTTCTTCTTAGCTCAAGACATT 360  
QY 361 AGTTCTTACTCATTAACAATTTGGTCTCATGAAGCTAAAAAATTAATGCCAGAGTGGT 420  
Db |||||||  
421 AGTTCTTACTCATTAACAATTTGGTCTCATGAAGCTAAAAAATTAATGCCAGAGTGGT 420  
QY 421 AGCATTGTTGCAACAACATATTTAGTGGCGCAATTCGCAGTTTCAAAATTTATAATGTGATG 480  
Db |||||||  
421 AGCATTGTTGCAACAACATATTTAGTGGCGCAATTCGCAGTTTCAAAATTTATAATGTGATG 480  
QY 481 GGTGTTGCTTAAAGCGAGCTTAGAAGCAAAATGTTAAATATTTAGCATTAGACTTAGTCTCT 540  
Db |||||||  
481 GGTGTTGCTTAAAGCGAGCTTAGAAGCAAAATGTTAAATATTTAGCATTAGACTTAGTCTCT 540  
QY 541 GATAATATTCGGTAAATGCAATTTACGCTGGTCCCAATTCGCTGATCAATTAAGTGCAAAAAGGT 600  
Db |||||||  
541 GATAATATTCGGTAAATGCAATTTACGCTGGTCCCAATTTACGCTGGTCCCAATTAAGTGCAAAAAGGT 600  
QY 601 GTGGGTGGTTCCTCAATACAATTTCTTAAAGAAATCGAAGAGCGTGCACCTTTAAAAAGCTAA 659  
Db |||||||  
601 GTGGGTGGTTCCTCAATACAATTTCTTAAAGAAATCGAAGAGCGTGCACCTTTAAAAAGCTAA 659

RESULT 6

US-10-138-701-5  
; Sequence 5, Application US/10138701  
; Publication No. US20030186364A1  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc. et al.  
; TITLE OF INVENTION: Staphylococcus aureus genes and polypeptides  
; FILE REFERENCE: PB484  
; CURRENT APPLICATION NUMBER: US/10/138,701  
; CURRENT FILING DATE: 2002-05-06  
; PRIOR APPLICATION NUMBER: US/09/512,255A  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/098,964  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: US 60/009,861  
; PRIOR FILING DATE: 1996-01-05  
; PRIOR APPLICATION NUMBER: PCT/ US99/19726  
; PRIOR FILING DATE: 1999-08-31  
; PRIOR APPLICATION NUMBER: US 08/956,171  
; PRIOR FILING DATE: 1997-10-20  
; NUMBER OF SEQ ID NOS: 61  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 5  
; LENGTH: 916

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; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-138-701-5

Query Match      65.6%; Score 506; DB 16; Length 916;
Best Local Similarity 99.5%; Pred. No. 5.1e-243;
Matches 656; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGTTAAATCTTGAACACAAAACATATGTCATCATGCGGAATCGCTAATAAGCGTAGTATT 60
Db ATGTTAAATCTTGAACACAAAACATATGTCATCATGCGGAATCGCTAATAAGCGTAGTATT 155
QY 61 GCTTTTGGTGCCTAAAGTTTGTAGATCAATTAGGTGCTCAATTTAGTATTACTTACCGT 120
Db GCTTTTGGTGCCTAAAGTTTGTAGATCAATTAGGTGCTCAATTTAGTATTACTTACCGT 215
QY 121 AAAGAACGTAGCCGTAAAGAGCTTGAAGAAATTAATTAGAACAAATTAATCAACAGAGCG 180
Db AAAGAACGTAGCCGTAAAGAGCTTGAAGAAATTAATTAGAACAAATTAATCAACAGAGCG 275
QY 181 CACTTATATCAAAATGATGTTCAAAGCGATGAAGGTTAATATGTTTGTAGCAAAAT 240
Db CACTTATATCAAAATGATGTTCAAAGCGATGAAGGTTAATATGTTTGTAGCAAAAT 335
QY 241 GGTAAAGATGTTGGCAATATGATGTTGATATCAATTCATCGCATTTGCTAATATGGAA 300
Db GGTAAAGATGTTGGCAATATGATGTTGATATCAATTCATCGCATTTGCTAATATGGAA 395
QY 301 GACTTACCGGAGCGCTTTCTGAAACTTCACGTGAAGGCTTCTTGTAGCTCAAGACATT 360
Db GACTTACCGGAGCGCTTTCTGAAACTTCACGTGAAGGCTTCTTGTAGCTCAAGACATT 455
QY 361 AGTCTTACTCATTAACAATTTGGCTCATGAAGCTAAAAAATTAATGCCAGAGTGGT 420
Db AGTCTTACTCATTAACAATTTGGCTCATGAAGCTAAAAAATTAATGCCAGAGTGGT 515
QY 421 AGCATTTGTCACACACATATTTAGTGGCGAATTCGCAAGTTCAAAATTAATATGTATG 480
Db AGCATTTGTCACACACATATTTAGTGGCGAATTCGCAAGTTCAAAATTAATATGTATG 575
QY 481 GGTGTTGCTAAAGCGAGCTTAGAAGCAATTTAAATATTTAGCATTTAGCTTAGTCCT 540
Db GGTGTTGCTAAAGCGAGCTTAGAAGCAATTTAAATATTTAGCATTTAGCTTAGTCCT 635
QY 541 GATAATATTCGCTTAATCAATTTTCAGTGGTCCAAATCCGTCACATTAAGTGCAAAAGGT 600
Db GATAATATTCGCTTAATCAATTTTCAGTGGTCCAAATCCGTCACATTAAGTGCAAAAGGT 695
QY 601 GTGGGTGGTTTCAATACAAATCTTAAGAAATCGAAGAGCGTGACCTTTAAAAACGTAA 659
Db GTGGGTGGTTTCAATACAAATCTTAAGAAATCGAAGAGCGTGACCTTTAAAAACGTAA 754

RESULT 7
US-10-823-785-5
; Sequence 5, Application US/10823785
; Publication No. US20040265962A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc. et al.
; TITLE OF INVENTION: Staphylococcus aureus genes and polypeptides
; FILE REFERENCE: PB484
; CURRENT APPLICATION NUMBER: US/10/823,785
; CURRENT FILING DATE: 2004-04-14
; PRIOR APPLICATION NUMBER: US/09/512,255
; PRIOR FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: US 60/098,964
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: US 60/009,861
; PRIOR FILING DATE: 1996-01-05
; PRIOR APPLICATION NUMBER: PCT/US99/19726
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: US 08/956,171
; PRIOR FILING DATE: 1997-10-20
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; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 916
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-823-785-5

Query Match      65.6%; Score 506; DB 20; Length 916;
Best Local Similarity 99.5%; Pred. No. 5.1e-243;
Matches 656; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGTTAAATCTTGAACACAAAACATATGTCATCATGCGGAATCGCTAATAAGCGTAGTATT 60
Db ATGTTAAATCTTGAACACAAAACATATGTCATCATGCGGAATCGCTAATAAGCGTAGTATT 155
QY 61 GCTTTTGGTGCCTAAAGTTTGTAGATCAATTAGGTGCTCAATTTAGTATTACTTACCGT 120
Db GCTTTTGGTGCCTAAAGTTTGTAGATCAATTAGGTGCTCAATTTAGTATTACTTACCGT 215
QY 121 AAAGAACGTAGCCGTAAAGAGCTTGAAGAAATTAATTAGAACAAATTAATCAACAGAGCG 180
Db AAAGAACGTAGCCGTAAAGAGCTTGAAGAAATTAATTAGAACAAATTAATCAACAGAGCG 275
QY 181 CACTTATATCAAAATGATGTTCAAAGCGATGAAGGTTAATATGTTTGTAGCAAAAT 240
Db CACTTATATCAAAATGATGTTCAAAGCGATGAAGGTTAATATGTTTGTAGCAAAAT 335
QY 241 GGTAAAGATGTTGGCAATATGATGTTGATATCAATTCATCGCATTTGCTAATATGGAA 300
Db GGTAAAGATGTTGGCAATATGATGTTGATATCAATTCATCGCATTTGCTAATATGGAA 395
QY 301 GACTTACCGGAGCGCTTTCTGAAACTTCACGTGAAGGCTTCTTGTAGCTCAAGACATT 360
Db GACTTACCGGAGCGCTTTCTGAAACTTCACGTGAAGGCTTCTTGTAGCTCAAGACATT 455
QY 361 AGTCTTACTCATTAACAATTTGGCTCATGAAGCTAAAAAATTAATGCCAGAGTGGT 420
Db AGTCTTACTCATTAACAATTTGGCTCATGAAGCTAAAAAATTAATGCCAGAGTGGT 515
QY 421 AGCATTTGTCACACACATATTTAGTGGCGAATTCGCAAGTTCAAAATTAATATGTATG 480
Db AGCATTTGTCACACACATATTTAGTGGCGAATTCGCAAGTTCAAAATTAATATGTATG 575
QY 481 GGTGTTGCTAAAGCGAGCTTAGAAGCAATTTAAATATTTAGCATTTAGCTTAGTCCT 540
Db GGTGTTGCTAAAGCGAGCTTAGAAGCAATTTAAATATTTAGCATTTAGCTTAGTCCT 635
QY 541 GATAATATTCGCTTAATCAATTTTCAGTGGTCCAAATCCGTCACATTAAGTGCAAAAGGT 600
Db GATAATATTCGCTTAATCAATTTTCAGTGGTCCAAATCCGTCACATTAAGTGCAAAAGGT 695
QY 601 GTGGGTGGTTTCAATACAAATCTTAAGAAATCGAAGAGCGTGACCTTTAAAAACGTAA 659
Db GTGGGTGGTTTCAATACAAATCTTAAGAAATCGAAGAGCGTGACCTTTAAAAACGTAA 754

RESULT 8
US-09-815-242-1952/c
; Sequence 1952, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; PROKARYOTES
; FILE REFERENCE: ELITRA.011A
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; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1952
; LENGTH: 552
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-09-815-242-1952

Query Match
Best Local Similarity 100.0%; Pred. No. 5.9e-218;
Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTTAAATCTTGAACCAAAACATATGTCATCATGCGGAATCGCTAAATAAGCGTAGTATT 60
Db 456 ATGTTAAATCTTGAACCAAAACATATGTCATCATGCGGAATCGCTAAATAAGCGTAGTATT 397

QY 61 GCTTTTGGTGCCTAAAGCTTTAGATCAATTTAGTGTCTAAATTTAGTATTACTTTACCGT 120
Db 396 GCTTTTGGTGCCTAAAGCTTTAGATCAATTTAGTGTCTAAATTTAGTATTACTTTACCGT 337

QY 121 AAAGAACGTAGCGGTAAAGAGCTTGAAAAATTTATTAGAACAAATTAATCAACAGAGCG 180
Db 336 AAAGAACGTAGCGGTAAAGAGCTTGAAAAATTTATTAGAACAAATTAATCAACAGAGCG 277

QY 181 CACTTATATCAAAATTGATGTTCAAGCGATGAAGAGGTTATTAAATGGTTTTCAGCAAAATT 240
Db 276 CACTTATATCAAAATTGATGTTCAAGCGATGAAGAGGTTATTAAATGGTTTTCAGCAAAATT 217

QY 241 GGTAAAGATGTTGGCAATATTTGATGTTATATCAATTCGCAATTTGCTTAATATGGA 300
Db 216 GGTAAAGATGTTGGCAATATTTGATGTTATATCAATTCGCAATTTGCTTAATATGGA 157

QY 301 GACTTACGCGGACGCTTTTCTGAACTTCACGTGAAGGCTTCTTGTAGCTCAAGACATT 360
Db 156 GACTTACGCGGACGCTTTTCTGAACTTCACGTGAAGGCTTCTTGTAGCTCAAGACATT 97

QY 361 AGTTCTTACTCATTAACAAATTTGCTCATCAAGCTTAABAAATTAATGCGAGAGGTTGT 420
Db 96 AGTTCTTACTCATTAACAAATTTGCTCATCAAGCTTAABAAATTAATGCGAGAGGTTGT 37

QY 421 AGCATTTGTGCAACACATATTTAGTGGCGAATTC 456
Db 36 AGCATTTGTGCAACACATATTTAGTGGCGAATTC 1

RESULT 9
US-09-815-242-1963/c
; Sequence 1963, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
```

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; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1963
; LENGTH: 552
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-09-815-242-1963

Query Match
Best Local Similarity 100.0%; Pred. No. 5.9e-218;
Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTTAAATCTTGAACCAAAACATATGTCATCATGCGGAATCGCTAAATAAGCGTAGTATT 60
Db 456 ATGTTAAATCTTGAACCAAAACATATGTCATCATGCGGAATCGCTAAATAAGCGTAGTATT 397

QY 61 GCTTTTGGTGCCTAAAGCTTTAGATCAATTTAGTGTCTAAATTTAGTATTACTTTACCGT 120
Db 396 GCTTTTGGTGCCTAAAGCTTTAGATCAATTTAGTGTCTAAATTTAGTATTACTTTACCGT 337

QY 121 AAAGAACGTAGCGGTAAAGAGCTTGAAAAATTTATTAGAACAAATTAATCAACAGAGCG 180
Db 336 AAAGAACGTAGCGGTAAAGAGCTTGAAAAATTTATTAGAACAAATTAATCAACAGAGCG 277

QY 181 CACTTATATCAAAATTGATGTTCAAGCGATGAAGAGGTTATTAAATGGTTTTCAGCAAAATT 240
Db 276 CACTTATATCAAAATTGATGTTCAAGCGATGAAGAGGTTATTAAATGGTTTTCAGCAAAATT 217

QY 241 GGTAAAGATGTTGGCAATATTTGATGTTATATCAATTCGCAATTTGCTTAATATGGA 300
Db 216 GGTAAAGATGTTGGCAATATTTGATGTTATATCAATTCGCAATTTGCTTAATATGGA 157

QY 301 GACTTACGCGGACGCTTTTCTGAACTTCACGTGAAGGCTTCTTGTAGCTCAAGACATT 360
Db 156 GACTTACGCGGACGCTTTTCTGAACTTCACGTGAAGGCTTCTTGTAGCTCAAGACATT 97

QY 361 AGTTCTTACTCATTAACAAATTTGCTCATCAAGCTTAABAAATTAATGCGAGAGGTTGT 420
Db 96 AGTTCTTACTCATTAACAAATTTGCTCATCAAGCTTAABAAATTAATGCGAGAGGTTGT 37

QY 421 AGCATTTGTGCAACACATATTTAGTGGCGAATTC 456
Db 36 AGCATTTGTGCAACACATATTTAGTGGCGAATTC 1

RESULT 10
US-10-282-122A-4490/c
; Sequence 4490, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
```

APPLICANT: Haselbeck, Robert  
APPLICANT: Ohlsen, Kari  
APPLICANT: Zyskind, Judith  
APPLICANT: Wall, Daniel  
APPLICANT: Trawick, John  
APPLICANT: Carr, Grant  
APPLICANT: Yamamoto, Robert  
APPLICANT: Forsyth, R.  
APPLICANT: Xu, H.  
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
FILE REFERENCE: ELITRA.034A  
CURRENT APPLICATION NUMBER: US/10/282,122A  
CURRENT FILING DATE: 2003-02-20  
PRIOR FILING DATE: 2000-03-21  
PRIOR FILING DATE: 2000-03-21  
PRIOR FILING DATE: 2000-05-23  
PRIOR FILING DATE: 2000-05-23  
PRIOR FILING DATE: 2000-07-27  
PRIOR FILING DATE: 2000-05-26  
PRIOR FILING DATE: 2000-09-06  
PRIOR FILING DATE: 2000-09-06  
PRIOR FILING DATE: 2000-11-27  
PRIOR FILING DATE: 2000-11-27  
PRIOR FILING DATE: 2000-12-22  
PRIOR FILING DATE: 2001-02-09  
PRIOR FILING DATE: 2001-02-16  
PRIOR FILING DATE: 2001-02-16  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 78614  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 4490  
LENGTH: 552  
TYPE: DNA  
ORGANISM: Staphylococcus aureus  
US-10-282-122A-4490

Query Match 59.1%; Score 456; DB 17; Length 552;  
Best Local Similarity 100.0%; Pred. No. 5.9e-218;  
Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTTAAATCTTGAACAAACATATGTCATCGGAATCGCTAATAAGCGTAGTATT 60  
DB 456 ATGTTAAATCTTGAACAAACATATGTCATCGGAATCGCTAATAAGCGTAGTATT 397

QY 61 GCTTTTGGTGTGCTAAAGTTTGTAGATCAATTAGGTGCTAAATAGTATTACTTACCGT 120  
DB 396 GCTTTTGGTGTGCTAAAGTTTGTAGATCAATTAGGTGCTAAATAGTATTACTTACCGT 337

QY 121 AAAGAACGTAGCGGTGCTAAAGTTTGTAGATCAATTAGGTGCTAAATAGTATTACTTACCGT 180  
DB 336 AAAGAACGTAGCGGTGCTAAAGTTTGTAGATCAATTAGGTGCTAAATAGTATTACTTACCGT 277

QY 181 CACTTATATCAATTAATGATGTTCAACGCGATGAAGGTTTATTAATGGTTTGTAGCAAAAT 240  
DB 276 CACTTATATCAATTAATGATGTTCAACGCGATGAAGGTTTATTAATGGTTTGTAGCAAAAT 217

QY 241 GGTAAAGATGTTGGCAATATGATGTTGTATATCAATTCATCGCATTTGCTAATATGAA 300  
DB 216 GGTAAAGATGTTGGCAATATGATGTTGTATATCAATTCATCGCATTTGCTAATATGAA 157

QY 301 GACTTACGGCGACGCTTTTCTGAAACTTCACTGTAAGGCTTCTTGTAGTCAAGACATT 360  
DB 156 GACTTACGGCGACGCTTTTCTGAAACTTCACTGTAAGGCTTCTTGTAGTCAAGACATT 97

QY 361 AGTCTTACTCATTAACAATTTGGTGTATGAAGCTTAAAGGTTTAAATTAATGCAAGGTTGT 420  
DB 96 AGTCTTACTCATTAACAATTTGGTGTATGAAGCTTAAAGGTTTAAATTAATGCAAGGTTGT 37

QY 421 AGCATTTGTCACCAACACATATTTAGTGCGCAATTC 456  
DB 36 AGCATTTGTCACCAACACATATTTAGTGCGCAATTC 1

RESULT 11  
US-10-282-122A-4491/c  
Sequence 4491, Application US/10282122A  
Publication No. US20040029129A1  
GENERAL INFORMATION:  
APPLICANT: Wang, Liangsu  
APPLICANT: Zamudio, Carlos  
APPLICANT: Malone, Cheryl  
APPLICANT: Haselbeck, Robert  
APPLICANT: Ohlsen, Kari  
APPLICANT: Zyskind, Judith  
APPLICANT: Wall, Daniel  
APPLICANT: Trawick, John  
APPLICANT: Carr, Grant  
APPLICANT: Yamamoto, Robert  
APPLICANT: Forsyth, R.  
APPLICANT: Xu, H.  
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
FILE REFERENCE: ELITRA.034A  
CURRENT APPLICATION NUMBER: US/10/282,122A  
CURRENT FILING DATE: 2003-02-20  
PRIOR APPLICATION NUMBER: 60/191,078  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: 60/206,848  
PRIOR FILING DATE: 2000-05-23  
PRIOR APPLICATION NUMBER: 60/207,727  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: 60/230,335  
PRIOR FILING DATE: 2000-09-06  
PRIOR APPLICATION NUMBER: 60/230,347  
PRIOR FILING DATE: 2000-09-09  
PRIOR APPLICATION NUMBER: 60/242,578  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/253,625  
PRIOR FILING DATE: 2000-11-27  
PRIOR APPLICATION NUMBER: 60/257,931  
PRIOR FILING DATE: 2000-12-22  
PRIOR APPLICATION NUMBER: 60/267,636  
PRIOR FILING DATE: 2001-02-09  
PRIOR APPLICATION NUMBER: 60/269,308  
PRIOR FILING DATE: 2001-02-16  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 78614  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 4491  
LENGTH: 552  
TYPE: DNA  
ORGANISM: Staphylococcus aureus  
US-10-282-122A-4491

Query Match 59.1%; Score 456; DB 17; Length 552;  
Best Local Similarity 100.0%; Pred. No. 5.9e-219;  
Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTTAAATCTTGAACAAACATATGTCATCGGAATCGCTAATAAGCGTAGTATT 60  
DB 456 ATGTTAAATCTTGAACAAACATATGTCATCGGAATCGCTAATAAGCGTAGTATT 397

QY 61 GCTTTTGGTGTGCTAAAGTTTGTAGATCAATTAGGTGCTAAATAGTATTACTTACCGT 120  
DB 396 GCTTTTGGTGTGCTAAAGTTTGTAGATCAATTAGGTGCTAAATAGTATTACTTACCGT 337

QY 121 AAAGAACGTAGCGGTGCTAAAGTTTGTAGATCAATTAGGTGCTAAATAGTATTACTTACCGT 180  
DB 336 AAAGAACGTAGCGGTGCTAAAGTTTGTAGATCAATTAGGTGCTAAATAGTATTACTTACCGT 277

QY 181 CACTTATATCAATTAATGATGTTCAACGCGATGAAGGTTTATTAATGGTTTGTAGCAAAAT 240



Db 276 CACTTATATCAAAATTTGATGTTCAAGAGCATGAAGAGGTTATTAATGTTTGGACAAATT 217  
QY 241 GGTAAAGATGTTGGCAATATTCATGCGTGTATATCATTCATGCGATTTGCTTAATATGGAA 300  
Db 216 GGTAAAGATGTTGGCAATATTCATGCGTGTATATCATTCATGCGATTTGCTTAATATGGAA 157  
QY 301 GACTTACGGGAGCGCTTTCTCAAACTTCACGTGAAGGCTTCTGTTAGCTCAAGACATT 360  
Db 156 GACTTACGGGAGCGCTTTCTGAAACTTCACGTGAAGGCTTCTGTTAGCTCAAGACATT 97  
QY 361 AGTTCTTACTCATTAAACAATTTGGCTCATGAAGCTAAAAAATTAATGCCAGAGGTGGT 420  
Db 96 AGTTCTTACTCATTAAACAATTTGGCTCATGAAGCTAAAAAATTAATGCCAGAGGTGGT 37  
QY 421 AGCATTTGTCACAAACATATTTAGTGGCGGAATTC 456  
Db 36 AGCATTTGTCACAAACATATTTAGTGGCGGAATTC 1

## RESULT 12

US-08-781-986A-772  
; Sequence 772, Application US/08781986A  
; Publication No. US20030054436A1  
; GENERAL INFORMATION:  
; APPLICANT: Charles Kunsch  
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences  
; NUMBER OF SEQUENCES: 5255  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Human Genome Sciences, Inc.  
; STREET: 9410 Key West Avenue  
; CITY: Rockville  
; STATE: Maryland  
; COUNTRY: USA  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
; COMPUTER: HP Vectra 486/33  
; OPERATING SYSTEM: MSDOS version 6.2  
; SOFTWARE: ASCII Text  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/781,986A  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Benson, Bob  
; REGISTRATION NUMBER: 30,446  
; REFERENCE/DOCKET NUMBER: PB248PP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (301) 309-8504  
; TELEFAX: (301) 309-8512  
; INFORMATION FOR SEQ ID NO: 772:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 704 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear

US-08-781-986A-772  
Query Match 56.7%; Score 437; DB 8; Length 704;  
Best Local Similarity 99.6%; Pred. No. 2.1e-208;  
Matches 537; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 ATGTTAAATCTTGAACCAACAAACATATGTCATCGGGAATCGCTTAATAAGCGTAGTATT 60  
Db 24 AIGTTAAATCTTGAACCAACAAACATATGTCATCGGGAATCGCTTAATAAGCGTAGTATT 83  
QY 61 GCTTTTGGTGTCCGCTAAAGTTTTAGATCAATTTAGGTGCTAAATAGTATTTACTTACCGT 120  
Db 84 GCTTTTGGTGTCCGCTAAAGTTTTAGATCAATTTAGGTGCTAAATAGTATTTACTTACCGT 143

QY 121 AAAGAACTAGCGCTAAAGAGCTTTGAAAAATTTATTAGAACAATTTAAATCAACCCAGAGCG 180  
Db 144 AAAGAACTAGCGCTAAAGAGCTTTGAAAAATTTATTAGAACAATTTAAATCAACCCAGAGCG 203  
QY 181 CACTTATATCAAAATTTGATGTTCAAAGCGATGAAGAGGTTATTAATGTTTGGACAAATT 240  
Db 204 CACTTATATCAAAATTTGATGTTCAAAGCGATGAAGAGGTTATTAATGTTTGGACAAATT 263  
QY 241 GGTAAAGATGTTGGCAATATTTGATGTTGATGTTGATATATCATTCATTCATTCGATTCGCTTAATATGGAA 300  
Db 264 GGTAAAGATGTTGGCAATATTTGATGTTGATGTTGATATATCATTCATTCATTCGATTCGCTTAATATGGAA 323  
QY 301 GACTTACGGGAGCGCTTTCTGAAACTTCACGTGAAGGCTTCTGTTAGCTCAAGACATT 360  
Db 324 GACTTACGGGAGCGCTTTCTGAAACTTCACGTGAAGGCTTCTGTTAGCTCAAGACATT 383  
QY 361 AGTTCTTACTCATTAAACAATTTGGCTCATGAAGCTAAAAAATTAATGCCAGAGGTGGT 420  
Db 384 AGTTCTTACTCATTAAACAATTTGGCTCATGAAGCTAAAAAATTAATGCCAGAGGTGGT 443  
QY 421 AGCATTTGTCACAAACATATTTAGTGGCGGAATTCGAGTTCAAATTAATATGTTGATG 480  
Db 444 AGCATTTGTCACAAACATATTTAGTGGCGGAATTCGAGTTCAAATTAATATGTTGATG 503  
QY 481 GGTGTTGCTAAAGCGAGCTTAGAAGCAAAATGCTTAAATATTTAGCATTAGACTTAGGTCC 539  
Db 504 GGTGTTGCTAAAGCGAGCTTAGAAGCAAAATGCTTAAATATTTAGCATTAGACTTAGGTCC 562

RESULT 13  
US-10-329-624-772  
; Sequence 772, Application US/10329624  
; Publication No. US20040043037A1  
; GENERAL INFORMATION:  
; APPLICANT: Charles Kunsch  
; Gil H. Choi  
; Patrick S. Dillon  
; Craig A. Rosen  
; Steven C. Barash  
; Michael R. Fannon  
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences  
; NUMBER OF SEQUENCES: 5256  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Human Genome Sciences, Inc.  
; STREET: 9410 Key West Avenue  
; CITY: Rockville  
; STATE: Maryland  
; COUNTRY: USA  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
; COMPUTER: HP Vectra 486/33  
; OPERATING SYSTEM: MSDOS version 6.2  
; SOFTWARE: ASCII Text  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/329,624  
; FILING DATE: 27-Dec-2002  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/956,171  
; FILING DATE: October 20, 1997  
; APPLICATION NUMBER: 60/009,861  
; FILING DATE: January 5, 1996  
; APPLICATION NUMBER: 08/781,986  
; FILING DATE: January 3, 1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mark J. Hyman  
; REGISTRATION NUMBER: 46,789  
; REFERENCE/DOCKET NUMBER: PB248P1D1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (240) 314-1224  
; TELEFAX: (301) 309-8439  
; INFORMATION FOR SEQ ID NO: 772:



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;
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 704 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: double
;   TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 772:
US-10-329-624-772

Query Match      56.7%; Score 437; DB 18; Length 704;
Best Local Similarity 99.6%; Pred. No. 2.1e-208;
Matches 537; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGTTAAATCTTGAACAAACAAACATATGTCATCATGCGGAATCGCTAATAAGCGTAGTATT 60
DB 24 ATGTTAAATCTTGAACAAACAAACATATGTCATCATGCGGAATCGCTAATAAGCGTAGTATT 83
QY 61 GCTTTTGGTCTGCTAAAGTTTGTAGATCAATAGGTGCTAAATAGTATTACTTACCGT 120
DB 84 GCTTTTGGTCTGCTAAAGTTTGTAGATCAATAGGTGCTAAATAGTATTACTTACCGT 143
QY 121 AAGAAAGCTAGCCGTGAAGAGCTTTGAAAAATTATTAGAACAAATTAATCAACCAAGGCG 180
DB 144 AAGAAAGCTAGCCGTGAAGAGCTTTGAAAAATTATTAGAACAAATTAATCAACCAAGGCG 203
QY 181 CACTTATATCAAAATTGATGTTCAAGCGATGAAGAGGTTAATTAATGGTTTGAAGCAAAAT 240
DB 204 CACTTATATCAAAATTGATGTTCAAGCGATGAAGAGGTTAATTAATGGTTTGAAGCAAAAT 263
QY 241 GGTAAAGATGTTGGCAATATTGATGTTATATCAATCGCATTTGCTTAATATATGGAA 300
DB 264 GGTAAAGATGTTGGCAATATTGATGTTATATCAATCGCATTTGCTTAATATATGGAA 323
QY 301 GACTTACGCGGAGCGCTTTTCTGAAACTTCAAGTGAAGGCTTCTTGTAGCTCAAGACATT 360
DB 324 GACTTACGCGGAGCGCTTTTCTGAAACTTCAAGTGAAGGCTTCTTGTAGCTCAAGACATT 383
QY 361 AGTCTTACTCATTAACAAATTGGCTCATGAAGCTTAAAAAATTAATGCCAAGGTGGT 420
DB 384 AGTCTTACTCATTAACAAATTGGCTCATGAAGCTTAAAAAATTAATGCCAAGGTGGT 443
QY 421 AGCATTTGTCACACACATATTAGGTGGCAATTCGCGATTCCAAATATATATGTATG 480
DB 444 AGCATTTGTCACACACATATTAGGTGGCAATTCGCGATTCCAAATATATATGTATG 503
QY 481 GGTGTTGCTTAAGCGAGCTTTAGAACCAAAATGTTAAATATTAGCATTTAGCTTGGTCC 539
DB 504 GGTGTTGCTTAAGCGAGCTTTAGAACCAAAATGTTAAATATTAGCATTTAGCTTGGTCC 562

RESULT 14
US-09-815-242-1697/c
; Sequence 1697, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011a
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
```

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;
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1697
; LENGTH: 324
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-09-815-242-1697

Query Match      42.0%; Score 324; DB 9; Length 324;
Best Local Similarity 100.0%; Pred. No. 9.5e-152;
Matches 324; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 135 TAAAGAGCTTGAATAATTATTAGAACAAATTAATCAACCAAGGCGCACTTATATCAAAAT 194
DB 324 TAAAGAGCTTGAATAATTATTAGAACAAATTAATCAACCAAGGCGCACTTATATCAAAAT 265
QY 195 TGATGTTCAAGCGATGAAGAGGTTAATTAATGGTTTGAAGCAAAATTTGGTAAAGATGTTGG 254
DB 264 TGATGTTCAAGCGATGAAGAGGTTAATTAATGGTTTGAAGCAAAATTTGGTAAAGATGTTGG 205
QY 255 CAATATTGATGTTATATCAATCGCATTTGCTTAATATGCTTAATATGGAAGACTTACGCGGACG 314
DB 204 CAATATTGATGTTATATCAATCGCATTTGCTTAATATGCTTAATATGGAAGACTTACGCGGACG 145
QY 315 CTTTCTGAAACTTCAAGTGAAGGCTTCTTGTAGCTCAAGACATTAGTTCTTACTCAATT 374
DB 144 CTTTCTGAAACTTCAAGTGAAGGCTTCTTGTAGCTCAAGACATTAGTTCTTACTCAATT 85
QY 375 ACAATTTGGCTCATGAAGCTTAAAAAATTAATGCCAAGGTGGTAGCATTTGTCGAAC 434
DB 84 ACAATTTGGCTCATGAAGCTTAAAAAATTAATGCCAAGGTGGTAGCATTTGTCGAAC 25
QY 435 ACATATTTAGTGGCGAATTCCG 458
DB 24 ACATATTTAGTGGCGAATTCCG 1

RESULT 15
US-09-815-242-3050/c
; Sequence 3050, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011a
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
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; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3050
; LENGTH: 324
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-09-815-242-3050

Query Match      42.0%; Score 324; DB 9; Length 324;
Best Local Similarity 100.0%; Pred. No. 9.5e-152; Indels 0; Gaps 0;
Matches 324; Conservative 0; Mismatches 0;

Qy 135 TAAAGAGCTTGA AAAATTATTAGAACAAATTAATCAACCAAGAGCGCACTTATATCAAAAT 194
Db      |||
Qy 324 TAAAGAGCTTGA AAAATTATTAGAACAAATTAATCAACCAAGAGCGCACTTATATCAAAAT 265
Db      |||
Qy 195 TGATGTTCAAGCGATGAAGAGGTTATTAAATGGTTTGGAGCAAAATGGTAAAGATGTTGG 254
Db      |||
Qy 264 TGATGTTCAAGCGATGAAGAGGTTATTAAATGGTTTGGAGCAAAATGGTAAAGATGTTGG 205
Db      |||
Qy 255 CAATATTGATGTTATATCAATCGCATTTGCTAATATGGAAGACTTACGGGACG 314
Db      |||
Qy 204 CAATATTGATGTTATATCAATCGCATTTGCTAATATGGAAGACTTACGGGACG 145
Db      |||
Qy 315 CTTTCTGAAACTTCACGTGAAGGCTTCTTGTAGCTCAAGACATTAGTTCTTACTCATT 374
Db      |||
Qy 144 CTTTCTGAAACTTCACGTGAAGGCTTCTTGTAGCTCAAGACATTAGTTCTTACTCATT 85
Db      |||
Qy 375 AACAAATTGGGCTCATGAAGCTAAAAAATTAATGCCAGAGGTGGTAGCATTTGGCAAC 434
Db      |||
Qy 84 AACAAATTGGGCTCATGAAGCTAAAAAATTAATGCCAGAGGTGGTAGCATTTGGCAAC 25
Db      |||
Qy 435 AACATATTTAGGTGGCAATTCGC 458
Db      |||
Qy 24 AACATATTTAGGTGGCAATTCGC 1
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Search completed: September 6, 2005, 14:29:14  
Job time : 4732 secs

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: September 6, 2005, 09:13:03 ; Search time 182 Seconds  
(without alignments)  
2301.576 Million cell updates/sec

Title: US-08-790-043B-2  
Perfect score: 256  
Sequence: 1 MLNLENTYVINGIANKRSI.....LSSGVGTGENIHVDSGFHAIK 256

Scoring table:  
OLIGO Xgapop 60.0 , Xgapext 60.0  
Ygapop 60.0 , Ygapext 60.0  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Word size: 1

Total number of hits satisfying chosen parameters: 2399978

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:

-MODEL=frame+p2n.model -DEV=xlp  
-O=/cgn2\_1/USPTO.spool\_p/US08790043/runat\_06092005\_101256\_4940/app.query.fasta\_1.455  
-DB=Issued Patents NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0 1 -LOOPL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US08790043 @CGN 1 1 105 @runat\_06092005\_101256\_4940 -NCPU=3  
-NO MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:\*  
1: /cgn2\_6/ptodata/1/ina/5A.COMB.seq.\*  
2: /cgn2\_6/ptodata/1/ina/5B.COMB.seq.\*  
3: /cgn2\_6/ptodata/1/ina/6A.COMB.seq.\*  
4: /cgn2\_6/ptodata/1/ina/6B.COMB.seq.\*  
5: /cgn2\_6/ptodata/1/ina/PTCUS.COMB.seq.\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	256	100.0	771	3	US-09-292-412-1
2	256	100.0	771	4	US-09-292-412-1
3	190	74.2	916	4	US-10-138-701-5
4	159	62.1	704	4	US-08-956-171B-772
5	159	62.1	704	4	US-08-781-986A-772
6	33	12.9	587	4	US-08-956-171B-514
7	33	12.9	587	4	US-08-781-986A-514
8	32	12.5	783	3	US-09-134-001C-1172
9	14	5.5	906	4	US-09-540-236-500
10	14	5.5	912	4	US-09-328-352-4085
11	14	5.5	65792	4	US-09-596-002-31
12	14	5.5	1830121	4	US-09-557-884-1

ALIGNMENTS

RESULT 1  
US-09-292-412-1  
; Sequence 1, Application US/09292412  
; Patent No. 6432670  
; GENERAL INFORMATION:  
; APPLICANT: Payne, David  
; APPLICANT: Lonsdale, John  
; APPLICANT: Milner, Peter  
; APPLICANT: Pearson, Stewart  
; TITLE OF INVENTION: FAB I  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dechert Price & Rhoads  
; STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre  
; CITY: Philadelphia  
; STATE: PA  
; COUNTRY: US  
; ZIP: 19103  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: FastSeq for Windows Version 2.0b  
; CURRENT APPLICATION NUMBER: US/09/292,412  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/790,043  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Falk, Stephen T  
; REGISTRATION NUMBER: 36,795  
; REFERENCE/DOCKET NUMBER: GMS0005  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 215-994-2488

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; TELEFAX: 215-994-2222
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 771 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-09-292-412-1

Alignment Scores:
Pred. No.: 3,64e-272 Length: 771
Score: 256.00 Matches: 256
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-08-790-043B-2 (1-256) x US-09-292-412-1 (1-771)

QY 1 MetLeuAsnLeuGluAsnLysThrTyrValIleMetGlyIleAlaAsnLysArgSerIle 20
DB 1 ATGTTAAATCTTGAACAAACAAACATATGTCATCATGGGAATCGCTAATAAAGCGTAGTATT 60

QY 21 AlaPheGlyValAlaLysValLeuAspGlnLeuGlyAlaLysLeuValPheThrTyrArg 40
DB 61 GCTTTTGGTGTGCTAAAGCTTTTAGATCAATTAGGTGCTAAATTAGTATTACTTACCGT 120

QY 41 LysGluArgSerArgLysGluLeuGluLysLeuLeuGluGlnLeuAsnGlnProGluAla 60
DB 121 AAAGAACGCTAGCGGTGAAGAGCTTGAACAAATTTATTAGAACAAATTAATCAACAGAGCG 180

QY 61 HisLeuTyrGlnIleAspValGlnSerAspGluGluValIleAsnGlyPheGluGlnIle 80
DB 181 CACTTATATCAAAATGATGTTCAAGCGATGAAGGTTATTAAATGGTTTTCAGCAAAAT 240

QY 81 GlyLysAspValGlyValIleAsnLysThrTyrHisSerIleAlaPheAlaAsnMetGlu 100
DB 241 GGTAAAGATGTTGGCAATATGATGCTATATCATTCATCGCATTTGCTTAATATGNA 300

QY 101 AspLeuArgGlyArgPheSerGluThrSerArgGlyGlyPheLeuLeuAlaGlnAspIle 120
DB 301 GACTTACGGGACGCTTTCTGAACTTCACGTGAAGGCTTCTTGTAGCTCAAGACATT 360

QY 121 SerSerTyrSerLeuThrIleValAlaHisGluAlaLysLysLeuMetProGluGly 140
DB 361 AGTTCTTACTATTAACAATTTGGCTCATGAAGCTTAAACAAATTAATGCGAAGGTGGT 420

QY 141 SerIleValAlaThrThrTyrLeuGlyGlyPheAlaValGlnAsnTyrAsnValMet 160
DB 421 AGCATTTGTTGCAACACATATTTAGGTGGCAATTCGCAGTTCAAAATTTAATATGTGATG 480

QY 161 GlyValAlaLysAlaSerLeuGluAlaAsnValLysTyrLeuAlaLeuAspLeuGlyPro 180
DB 481 GGTGTGTCTAAAGCGAGCTTAGAAGCAAAATGTTAAATATTAGCATTAGCTTAGCTCT 540

QY 181 AspAsnIleArgValAsnAlaIleSerAlaGlyProIleArgThrLeuSerAlaLysGly 200
DB 541 GATAATATTCGGGTAAATCAATTTAGCTGTCAATCCGACATTAAGTCGCAAAAGGT 600

QY 201 ValGlyGlyPheAsnThrIleLeuLysGluIleGluGluArgAlaProLeuLysArgAsn 220
DB 601 GTGGGTGGTTTCAATACATTTCTTAAAGAAATCGAAGCGGTGCACCTTTTAAACGTAAC 660

QY 221 ValAspGlnValGluValGlyLysThrAlaAlaTyrLeuLeuSerAspLeuSerGly 240
DB 661 GTTGATCAAGTAGAAGTAGGTAAAAACAGCGGCTTACTTTRTTAAGTCACTTATCAAGTGGC 720

QY 241 ValThrGlyLysAlaIleHisValAspSerGlyPheHisAlaIleIys 256
DB 721 GTTACAGGTGAATAATATTATCATGTAGATACGGATTCCACGCAATTAATA 768
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US-09-292-411A-1
; Sequence 1, Application US/09292411A
; Patent No. 6753172
; GENERAL INFORMATION:
; APPLICANT: Lonsdale, John
; APPLICANT: Milner, Peter
; APPLICANT: Payne, David
; APPLICANT: Pearson, Stewart
; TITLE OF INVENTION: Fdri
; FILE REFERENCE: GMS0005-D1
; CURRENT APPLICATION NUMBER: US/09/292,411A
; CURRENT FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: US 08/790,043
; PRIOR FILING DATE: 1997-01-28
; PRIOR APPLICATION NUMBER: US 60/024,845
; PRIOR FILING DATE: 1996-08-26
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 771
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-09-292-411A-1

Alignment Scores:
Pred. No.: 3,64e-272 Length: 771
Score: 256.00 Matches: 256
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-08-790-043B-2 (1-256) x US-09-292-411A-1 (1-771)

QY 1 MetLeuAsnLeuGluAsnLysThrTyrValIleMetGlyIleAlaAsnLysArgSerIle 20
DB 1 ATGTTAAATCTTGAACAAACAAACATATGTCATCATGGGAATCGCTAATAAAGCGTAGTATT 60

QY 21 AlaPheGlyValAlaLysValLeuAspGlnLeuGlyAlaLysLeuValPheThrTyrArg 40
DB 61 GCTTTTGGTGTGCTAAAGCTTTTAGATCAATTAGGTGCTAAATTAGTATTACTTACCGT 120

QY 41 LysGluArgSerArgLysGluLeuGluLysLeuLeuGluGlnLeuAsnGlnProGluAla 60
DB 121 AAAGAACGCTAGCGGTGAAGAGCTTGAACAAATTTATTAGAACAAATTAATCAACAGAGCG 180

QY 61 HisLeuTyrGlnIleAspValGlnSerAspGluGluValIleAsnGlyPheGluGlnIle 80
DB 181 CACTTATATCAAAATGATGTTCAAGCGATGAAGGTTATTAAATGGTTTTCAGCAAAAT 240

QY 81 GlyLysAspValGlyValIleAsnLysThrTyrHisSerIleAlaPheAlaAsnMetGlu 100
DB 241 GGTAAAGATGTTGGCAATATGATGCTATATCATTCATCGCATTTGCTTAATATGNA 300

QY 101 AspLeuArgGlyArgPheSerGluThrSerArgGlyGlyPheLeuLeuAlaGlnAspIle 120
DB 301 GACTTACGGGACGCTTTCTGAACTTCACGTGAAGGCTTCTTGTAGCTCAAGACATT 360

QY 121 SerSerTyrSerLeuThrIleValAlaHisGluAlaLysLysLeuMetProGluGly 140
DB 361 AGTTCTTACTATTAACAATTTGGCTCATGAAGCTTAAACAAATTAATGCGAAGGTGGT 420

QY 141 SerIleValAlaThrThrTyrLeuGlyGlyPheAlaValGlnAsnTyrAsnValMet 160
DB 421 AGCATTTGTTGCAACACATATTTAGGTGGCAATTCGCAGTTCAAAATTTAATATGTGATG 480

QY 161 GlyValAlaLysAlaSerLeuGluAlaAsnValLysTyrLeuAlaLeuAspLeuGlyPro 180
DB 481 GGTGTGTCTAAAGCGAGCTTAGAAGCAAAATGTTAAATATTAGCATTAGCTTAGCTCT 540

QY 181 AspAsnIleArgValAsnAlaIleSerAlaGlyProIleArgThrLeuSerAlaLysGly 200
DB 541 GATAATATTCGGGTAAATCAATTTAGCTGTCAATCCGACATTAAGTCGCAAAAGGT 600
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Qy 201 ValGlyGlyPheAsnThrIleLeuLysGluIleGluGluArgAlaProLeuLysArgAsn 220  
Db 601 GTGGGTGTTTCAATCAATTTAAAGAAATCGAAGCGGTGCACCTTTAAAAACGTAAC 660  
Qy 221 ValAspGlnValGluValGlyValThrAlaAlaTyrIleuLeuSerAspLeuSerSerGly 240  
Db 661 GTTGATCAGTAGAAGTAGGTAACACGCGCTTACTTTRTAGTGACCTTATCAAGTGGC 720  
Qy 241 ValThrGlyGluAsnIleHisValAspSerGlyPheHisAlaIleLys 256  
Db 721 GTTACAGGTGAAATAATTATCATGTAGATAGCGGATTCACGCAATTAAA 768

RESULT 3  
US-10-138-701-5  
; Sequence 5, Application US/10138701  
; Patent No. 6753149  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc. et al.  
; TITLE OF INVENTION: Staphylococcus aureus genes and polypeptides  
; FILE REFERENCE: PB484  
; CURRENT APPLICATION NUMBER: US/10/138,701  
; PRIOR FILING DATE: 2002-05-06  
; PRIOR FILING DATE: US/09/512,255A  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/098,964  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: US 60/009,861  
; PRIOR FILING DATE: 1996-01-05  
; PRIOR APPLICATION NUMBER: PCT/ US99/19726  
; PRIOR FILING DATE: 1999-08-31  
; PRIOR APPLICATION NUMBER: US 08/956,171  
; PRIOR FILING DATE: 1997-10-20  
; NUMBER OF SEQ ID NOS: 61  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 5  
; LENGTH: 916  
; TYPE: DNA  
; ORGANISM: Staphylococcus aureus  
US-10-138-701-5

Alignment Scores:  
Pred. No.: 1.94e-199 Length: 916  
Score: 190.00 Matches: 255  
Percent Similarity: 99.22% Conservative: 0  
Best Local Similarity: 99.22% Mismatches: 1  
Query Match: 74.22% Indels: 2  
DB: 4 Gaps: 0

US-08-790-043B-2 (1-256) x US-10-138-701-5 (1-916)  
Qy 1 MetLeuAsnLeuGluAsnLysThrTyrValIleMetGlyIleAlaAsnLysArgSerIle 20  
Db 96 ATGTTAAATCTTGAAACAACAACATATGTCATCATGGAATCCGTAATAGCGTAGTATT 155  
Qy 21 AlaPheGlyValAlaLysValLeuAspGlnLeuGlyAlaLysLeuValPheThrTyrArg 40  
Db 156 GCITTTGGTGTGCTAAAGTTTTAGATCAATTAGGTGCTAAATAGTATTACTTACCGT 215  
Qy 41 LysGluArgSerArgLysGluLeuGlyLeuLeuGluGlnLeuAsnGlnProGluAla 60  
Db 216 AAAGAACGTAGCGCGTAAGAGCTTGAAATAATTATTAGACAATTAATCAACAGAACG 275  
Qy 61 HisLeuTyrGlnIleAspValGlnSerAspGluValIleAsnGlyPheGluGlnIle 80  
Db 276 CACTTATATCAATATTGATGTTCAAGCGATGAAGAGTTAATGTTTTAGCAAAAT 335  
Qy 81 GlyLysAspValGlyAsnIleAspGlyValTyrHisSerIleAlaPheAlaAsnMetGlu 100  
Db 336 GGTAAAGATGTTGCAATATTGATGGTGATATATCAATCAATCGAATTGCTAATATGGA 395  
Qy 101 AspLeuArgGlyArgPheSerGluThrSerArgGluGlyPheLeuLeuAlaGlnAspIle 120

Db 396 GACTTAGCGGACGCTTTTCTGAACTTCACGTGAAGGCTTCTTTGTAGCTCAAGACATT 455  
Qy 121 SerSerTyrSerLeuThrIleValAlaHisGluAlaLysLysLeuMetProGluGlyGly 140  
Db 456 AGTTCTTACTATTAAACAATTTGGCTCATGAAGCTAAAAAATTAATGCCAGAAGGTGGT 515  
Qy 141 SerIleValAlaThrThrTyrIleuGlyGlyGluPheAlaValGlnAsnTyrAsnValMet 160  
Db 516 AGCATTGTTGCAACAACATATTTAGTGGCGAATTCGCAAGTTCCAAACTATATAATGTGATG 575  
Qy 161 GlyValAlaLysAlaSerLeuGluAlaAsnValLysTyrLeuAlaLeuAspLeuGlyPro 180  
Db 576 GGTGTTGCTAAGCGAGCTTAGNAGCAATGTTAAATATATTAGCATTAGACTTAGGTCCA 635  
Qy 181 AspAsnIleArgValAsnAlaIleSerAlaGly-ProIleArgThrLeuSerAlaLysG1 200  
Db 636 GATAATATTCCGCTTAATGCAATTTTCAGCTAG-TCCAATCCGTACATTAAAGTCAAAAGG 694  
Qy 200 YValGlyGlyPheAsnThrIleLeuLysGluIleGluGluArgAlaProLeuLysArgAs 220  
Db 695 TGTGGGTGGTTCATATACAATTTCTTAAAGAAATCGAAGACGCGTGCACCTTTAAACGTAA 754  
Qy 220 nValAspGlnValGluValGlyLysThrAlaAlaTyrLeuLeuSerAspLeuSerSerG1 240  
Db 755 TGTGATCAAGTAGAAGTAGGTAAGTAAACTCGCGCTTACTTATTAAAGTATTATCAAGTGG 814  
Qy 240 YValThrGlyGluAsnIleHisValAspSerGlyPheHisAlaIleLys 256  
Db 815 CGTTACAGGTGAAATATTTTCATGTAGTAGCGGATTTCCACGCAATTAAA 863

RESULT 4  
US-08-956-171B-772  
; Sequence 772, Application US/08956171E  
; Patent No. 6593114  
; GENERAL INFORMATION:  
; APPLICANT: Charles Kunsch  
; Gil H. Choi  
; Patrick S. Dillon  
; Craig A. Rosen  
; Steven C. Barash  
; Michael R. Fannon  
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences  
; NUMBER OF SEQUENCES: 5256  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Human Genome Sciences, Inc.  
; STREET: 9410 Key West Avenue  
; CITY: Rockville  
; STATE: Maryland  
; COUNTRY: USA  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
; COMPUTER: HP Vectra 486/33  
; OPERATING SYSTEM: MSDOS version 6.2  
; SOFTWARE: ASCII Text  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/956,171E  
; FILING DATE: 20-Oct-1997  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/009,861  
; FILING DATE: January 5, 1996  
; APPLICATION NUMBER: 08/781,986  
; FILING DATE: January 3, 1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mark J. Hyman  
; REGISTRATION NUMBER: 46,789  
; REFERENCE/DOCKET NUMBER: PB248P1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (240) 314-1224  
; TELEFAX: (301) 309-8439  
; INFORMATION FOR SEQ ID NO: 772:  
; SEQUENCE CHARACTERISTICS:

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;
; LENGTH: 704 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 772:
US-08-956-171E-772

Alignment Scores:
Pred. No.: 1,97e-165 Length: 704
Score: 159.00 Matches: 189
Percent Similarity: 98.95% Conservative: 0
Best Local Similarity: 98.95% Mismatches: 1
Query Match: 62.11% Indels: 2
DB: 4 Gaps: 0

US-08-790-043B-2 (1-256) x US-08-956-171E-772 (1-704)

QY 1 MetLeuAsnLeuGluAsnLysThrTyrValIleMetGlyIleAlaAsnLysArgSerIle 20
Db 24 ATGTTAAATCTTGAAACAAACAAACATATGTCATCGGAATCGCTAAATAAGCGTAGTATT 83
QY 21 AlaPheGlyValAlaLysValLeuAspGlnLeu-GlyAlaLysLeuValPheThrTyrAr 40
Db 84 GCTTTTGGTGTGCGTAAAGCTTTTAGATCAATT-MGGTGTCTAAATTTAGTATTACTTACCG 142
QY 40 GlySerGluArgSerArgGlyLeuGluLysLeuLeuGluGlnLeuAsnGlnProGluAl 60
Db 143 TAAAGAACGTAGCCGTAAGAGCTTGAAAAATTTATTAGAACAAATTTAAATCAACCAAGAGC 202
QY 60 aHisLeuTyrGlnIleAspValGlnSerAspGlyValTyrHisSerIleAlaPheAlaAsnMetGl 100
Db 263 TGGTAAAGATGTTGGCAATATTGATGTTTCAAGCGATGAGAGGTTATTATGCTTTGACCAAT 322
QY 100 uAspLeuArgGlyArgPheSerGluThrSerArgGlyGlyPheLeuAlaGlnAspIle 120
Db 323 AGACTTACGCGAGCGCTTTTCTGAAACTTCACGTGAAGGCTTCTTTGTAGCTCAAGACAT 382
QY 120 eSerSerTyrSerLeuThrIleValAlaHisGluAlaLysLysLeuMetProGluGlyGl 140
Db 383 TAGTTCTTACTATTAAACAATTTGGCTCATGAGCTTAAAAATTTAATGCCAGAGGTGG 442
QY 140 ySerIleValAlaThrThrTyrLeuGlyGlyPheAlaValGlnAsnTyrAsnValMe 160
Db 443 TAGCATTGTTGCAACAACATATTAGGTGGCGAATTCGCAGTTCAAAACTATAATGTGAT 502
QY 160 tGlyValAlaLysAlaSerLeuGluAlaAsnValLysTyrLeuAlaLeuAspLeuGlyPr 180
Db 503 GGGTGTTCGTAAGCGAGCTTAGAGCAAAATGTTAAATATTATTAGCATTTAGACTTAGGTCC 562
QY 180 oAspAsnIleArgValAsnAlaIleSerAla 190
Db 563 AGATAATATTCGGTTAATGCAATTTTCAGCT 593

RESULT 5
US-08-781-986A-772
; Sequence 772, Application US/08781986A
; Patent No. 6737248
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
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;
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PB248PP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 772:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 704 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-781-986A-772

Alignment Scores:
Pred. No.: 1,97e-165 Length: 704
Score: 159.00 Matches: 189
Percent Similarity: 98.95% Conservative: 0
Best Local Similarity: 98.95% Mismatches: 1
Query Match: 62.11% Indels: 2
DB: 4 Gaps: 0

US-08-790-043B-2 (1-256) x US-08-781-986A-772 (1-704)

QY 1 MetLeuAsnLeuGluAsnLysThrTyrValIleMetGlyIleAlaAsnLysArgSerIle 20
Db 24 ATGTTAAATCTTGAAACAAACAAACATATGTCATCGGAATCGCTAAATAAGCGTAGTATT 83
QY 21 AlaPheGlyValAlaLysValLeuAspGlnLeu-GlyAlaLysLeuValPheThrTyrAr 40
Db 84 GCTTTTGGTGTGCGTAAAGCTTTTAGATCAATT-MGGTGTCTAAATTTAGTATTACTTACCG 142
QY 40 GlySerGluArgSerArgGlyLeuGluLysLeuLeuGluGlnLeuAsnGlnProGluAl 60
Db 143 TAAAGAACGTAGCCGTAAGAGCTTGAAAAATTTATTAGAACAAATTTAAATCAACCAAGAGC 202
QY 60 aHisLeuTyrGlnIleAspValGlnSerAspGlyValIleAsnGlyPheGluGlnIle 80
Db 203 GCACCTTATATCAATTTGATGTTTCAAGCGATGAGAGGTTATTATGCTTTGACCAAT 262
QY 80 eGlyLysAspValGlyAsnIleAspGlyValTyrHisSerIleAlaPheAlaAsnMetGl 100
Db 263 TGGTAAAGATGTTGGCAATATTGATGTTTCAATTCGATATCAATTCGATTTGCTTAATGGA 322
QY 100 uAspLeuArgGlyArgPheSerGluThrSerArgGlyGlyPheLeuAlaGlnAspIle 120
Db 323 AGACTTACGCGAGCGCTTTTCTGAAACTTCACGTGAAGGCTTCTTTGTAGCTCAAGACAT 382
QY 120 eSerSerTyrSerLeuThrIleValAlaHisGluAlaLysLysLeuMetProGluGlyGl 140
Db 383 TAGTTCTTACTATTAAACAATTTGGCTCATGAGCTTAAAAATTTAATGCCAGAGGTGG 442
QY 140 ySerIleValAlaThrThrTyrLeuGlyGlyPheAlaValGlnAsnTyrAsnValMe 160
Db 443 TAGCATTGTTGCAACAACATATTAGGTGGCGAATTCGCAGTTCAAAACTATAATGTGAT 502
QY 160 tGlyValAlaLysAlaSerLeuGluAlaAsnValLysTyrLeuAlaLeuAspLeuGlyPr 180
Db 503 GGGTGTTCGTAAGCGAGCTTAGAGCAAAATGTTAAATATTATTAGCATTTAGACTTAGGTCC 562
QY 180 oAspAsnIleArgValAsnAlaIleSerAla 190
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DB 563 AGATAATATTCGGTGAATGCAATTCAGCT 593  
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## RESULT 6

US-08-956-171E-514/c

; Sequence 514, Application US/08956171E

; Patent No. 6593114

; GENERAL INFORMATION:

; APPLICANT: Charles Kunsch

; Gil H. Choi

; Patrick S. Dillon

; Craig A. Rosen

; Steven C. Barash

; Michael R. Fannon

; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

; NUMBER OF SEQUENCES: 5256

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Human Genome Sciences, Inc.

; STREET: 9410 Key West Avenue

; CITY: Rockville

; STATE: Maryland

; COUNTRY: USA

; ZIP: 20850

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage

; COMPUTER: HP Vectra 486/33

; OPERATING SYSTEM: MSDOS version 6.2

; SOFTWARE: ASCII Text

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/956,171E

; FILING DATE: 20-Oct-1997

; CLASSIFICATION: &lt;Unknown&gt;

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 60/009,861

; FILING DATE: January 5, 1996

; APPLICATION NUMBER: 08/781,986

; FILING DATE: January 3, 1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Mark J. Hyman

; REGISTRATION NUMBER: 46,789

; REFERENCE/DOCKET NUMBER: PB248P1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (240) 314-1224

; TELEFAX: (301) 309-8439

; INFORMATION FOR SEQ ID NO: 514:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 587 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; SEQUENCE DESCRIPTION: SEQ ID NO: 514:

US-08-956-171E-514

## Alignment Scores:

Pred. No.:	8,16e-27	Length:	587
Score:	33.00	Matches:	33
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	12.89%	Indels:	0
DB:	4	Gaps:	0

US-08-790-043B-2 (1-256) x US-08-956-171E-514 (1-587)

QY 224 ValGluValGlyThrAlaAlaTyrLeuLeuSerAspLeuSerSerGlyValThrGly 243

DB 586 GTAGAAGTAGGTAAACCTCGGCTTACTTATTAAAGTGATTATCAAGTGGCGTTACAGT 527

QY 244 GluAenIleHisValAspSerGlyPheHisAlaIleLys 256

DB 526 GAAATATTTCATGTAGATAGCGGATTCACGCAATTTAAA 488

## RESULT 7

US-08-781-986A-514/c

; Sequence 514, Application US/08781986A

; Patent No. 6737248

; GENERAL INFORMATION:

; APPLICANT: Charles Kunsch

; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

; NUMBER OF SEQUENCES: 5255

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Human Genome Sciences, Inc.

; STREET: 9410 Key West Avenue

; CITY: Rockville

; STATE: Maryland

; COUNTRY: USA

; ZIP: 20850

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage

; COMPUTER: HP Vectra 486/33

; OPERATING SYSTEM: MSDOS version 6.2

; SOFTWARE: ASCII Text

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/781,986A

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Benson, Bob

; REGISTRATION NUMBER: 30,446

; REFERENCE/DOCKET NUMBER: PB248PP

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (301) 309-8504

; TELEFAX: (301) 309-8512

; INFORMATION FOR SEQ ID NO: 514:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 587 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

US-08-781-986A-514

## Alignment Scores:

Pred. No.:	8,16e-27	Length:	587
Score:	33.00	Matches:	33
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	12.89%	Indels:	0
DB:	4	Gaps:	0

US-08-790-043B-2 (1-256) x US-08-781-986A-514 (1-587)

QY 224 ValGluValGlyThrAlaAlaTyrLeuLeuSerAspLeuSerSerGlyValThrGly 243

DB 586 GTAGAAGTAGGTAAACCTCGGCTTACTTATTAAAGTGATTATCAAGTGGCGTTACAGT 527

QY 244 GluAenIleHisValAspSerGlyPheHisAlaIleLys 256

DB 526 GAAATATTTCATGTAGATAGCGGATTCACGCAATTTAAA 488

## RESULT 8

US-09-134-001C-1172

; Sequence 1172, Application US/09134001C

; Patent No. 6380370

; GENERAL INFORMATION:

; APPLICANT: Lynn Doucette-Stamm et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

; FILE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: GTC-007

; CURRENT APPLICATION NUMBER: US/09/134,001C

; CURRENT FILING DATE: 1998-08-13

; PRIOR APPLICATION NUMBER: US 60/064,964

; PRIOR FILING DATE: 1997-11-08

; PRIOR APPLICATION NUMBER: US 60/055,779

; PRIOR FILING DATE: 1997-08-14

```
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 1172
; LENGTH: 783
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-1172

Alignment Scores:
Pred. No.: 1.38e-25 Length: 783
Score: 32.00 Matches: 59
Percent Similarity: 96.72% Conservative: 0
Best Local Similarity: 96.72% Mismatches: 1
Query Match: 12.50% Indels: 2
DB: 3 Gaps: 0

US-08-790-043B-2 (1-256) x US-09-134-001C-1172 (1-783)

QY 153 AlaValGlnAsnTyrAsnValMetGlyValAlaLysAlaSerLeuGluAlaAsnValLys 172
DB 469 GCAGTTCAAAACATAATGTTATGGGTAGCTAAGCAAGTTTAGAGCGGATGTTAAA 528

QY 173 TyrLeuAlaLeuAspLeuGlyPro-AspAsnIleArgValAsnAlaIleSerAlaGlyPr 192
DB 529 TATTTAGCTTTAGACTTAGGTGA-AGATAAATATTCGTGTCRAATGCTATTTCTGCAGGGCC 587

QY 192 oileArgThrIeuSerAlaLysGlyValGlyGlyPheAsnThrIleLeuLysGluIleGl 212
DB 588 AATTCGTACTTTAAGTGCTAAAGGTAGGTGGATTTAATACAATTTCTTAAAGAAATTGA 647

QY 212 u 212
DB 648 A 648

RESULT 9
US-09-540-236-500
; Sequence 500, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARRHALIS
; FILE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 500
; LENGTH: 906
; TYPE: DNA
; ORGANISM: M. catarrhalis
US-09-540-236-500

Alignment Scores:
Pred. No.: 1.04e-05 Length: 906
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.47% Indels: 0
DB: 4 Gaps: 0

US-08-790-043B-2 (1-256) x US-09-540-236-500 (1-906)

QY 183 IleArgValAsnAlaIleSerAlaGlyProIleArgThrLeu 196
DB 640 ATTGCTGTCATAGCCATCAGTCAGGCGCCCTATCCGACGCTG 681

RESULT 10
US-09-328-352-4085
; Sequence 4085, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: 60/140,121
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PERL Program
; SEQ ID NO 31
; LENGTH: 65792
; TYPE: DNA
; ORGANISM: M. catarrhalis
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte template ID No. 6632636 31
; PUBLICATION INFORMATION:
US-09-596-002-31

Alignment Scores:
Pred. No.: 0.000799 Length: 65792
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.47% Indels: 0
DB: 4 Gaps: 0

US-08-790-043B-2 (1-256) x US-09-596-002-31 (1-65792)

QY 183 IleArgValAsnAlaIleSerAlaGlyProIleArgThrLeu 196
DB 32004 ATTGCTGTCATAGCCATCAGTCAGGCGCCCTATCCGACGCTG 32045

RESULT 12
US-09-557-884-1/c
; Sequence 1, Application US/09557884
; Patent No. 6506581
; GENERAL INFORMATION:
; APPLICANT: Fleischmann et al.
; TITLE OF INVENTION: The Nucleotide sequence of the Haemophilus influenzae Rd Genome, Fragments Thereof, and Uses Thereof
```



NUMBER OF SEQUENCES: 1  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: MD  
COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3 1/2 inch diskette  
COMPUTER: Dell Pentium  
OPERATING SYSTEM: MS DOS v6.22  
SOFTWARE: ASCII Text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/557,884  
FILING DATE: 25-Apr-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/476,102  
FILING DATE: JUN-5-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Michelle S. Marks  
REGISTRATION NUMBER: 41,971  
REFERENCE/DOCKET NUMBER: PB186P3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 301-309-8504  
TELEFAX: 301-309-8439  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1830121 base pairs  
TYPE: nucleic acid  
STRADEDNESS: double  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-557-884-1

Alignment Scores:  
Pred. No.: 0.0232 Length: 1830121  
Score: 14.00 Matches: 14  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 5.47% Indels: 0  
DB: 4 Gaps: 0

US-08-790-043B-2 (1-256) x US-09-557-884-1 (1-1830121)

Qy 183 ileArgValAsnAlaIleSerAlaGlyProIleArgThrLeu 196  
|||||  
Db 1810914 ATTCGTGTGAATGCAATCTCTGCAGGCCCAATCCGACCCTA 1810873

RESULT 13  
US-09-643-990A-1/c  
Sequence 1, Application US/09643990A  
Patent No. 6528289  
GENERAL INFORMATION:  
APPLICANT: Robert D. Fleischmann  
Mark D. Adams  
Owen White  
Hamilton O. Smith  
J. Craig Venter  
TITLE OF INVENTION: The Nucleotide sequence of the Haemophilus influenzae Rd Genome, Fragments Thereof, and Uses Thereof

NUMBER OF SEQUENCES: 1  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville,  
STATE: MD  
COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3 1/2 inch diskette

COMPUTER: Dell Pentium  
OPERATING SYSTEM: MS DOS v6.22  
SOFTWARE: ASCII Text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/643,990A  
FILING DATE: 23-Aug-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/487,429  
FILING DATE: 1995-06-07  
APPLICATION NUMBER: 08/426,787  
FILING DATE: 1995-04-21  
ATTORNEY/AGENT INFORMATION:  
NAME: Kenley K. Hoover  
REGISTRATION NUMBER: 40,302  
REFERENCE/DOCKET NUMBER: PB186PIC1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 301-610-5790  
TELEFAX: 310-309-8439  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1830121 base pairs  
TYPE: nucleic acid  
STRADEDNESS: double  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-643-990A-1

Alignment Scores:  
Pred. No.: 0.0232 Length: 1830121  
Score: 14.00 Matches: 14  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 5.47% Indels: 0  
DB: 4 Gaps: 0

US-08-790-043B-2 (1-256) x US-09-643-990A-1 (1-1830121)

Qy 183 ileArgValAsnAlaIleSerAlaGlyProIleArgThrLeu 196  
|||||  
Db 1810914 ATTCGTGTGAATGCAATCTCTGCAGGCCCAATCCGACCCTA 1810873

RESULT 14  
US-09-489-039A-768  
Sequence 768, Application US/09489039A  
Patent No. 6610836  
GENERAL INFORMATION:  
APPLICANT: Gary Breton et. al  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 2709.2004001  
CURRENT APPLICATION NUMBER: US/09/489,039A  
CURRENT FILING DATE: 2000-01-27  
PRIOR APPLICATION NUMBER: US 60/117,747  
PRIOR FILING DATE: 1999-01-29  
NUMBER OF SEQ ID NOS: 14342  
SEQ ID NO 768  
LENGTH: 813  
TYPE: DNA  
ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-768

Alignment Scores:  
Pred. No.: 0.000118 Length: 813  
Score: 13.00 Matches: 13  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 5.08% Indels: 0  
DB: 4 Gaps: 0

US-08-790-043B-2 (1-256) x US-09-489-039A-768 (1-813)

Qy 184 ArgValAsnAlaIleSerAlaGlyProIleArgThrLeu 196

```
Db          571 CGCGTCAATGCCATCTCTGCCGCTCTATCCGTACGCTG 609
|||||
RESULT 15
US-10-089-740-1
; Sequence 1, Application US/10089740
; Patent No. 6730684
; GENERAL INFORMATION:
; APPLICANT: Miller, William H.
; APPLICANT: Newlander, Kenneth A.
; APPLICANT: Seefeld, Mark A.
; APPLICANT: Uzinskas, Irene N.
; TITLE OF INVENTION: Fab I Inhibitors
; FILE REFERENCE: P51038
; CURRENT APPLICATION NUMBER: US/10/089,740
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: 60/158,707
; PRIOR FILING DATE: 1999-10-08
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 39
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-089-740-1

Alignment Scores:
Pred. No.:      0.0109      Length:      39
Score:          10.00      Matches:     10
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches:  0
Query Match:      3.91%      Indels:      0
DB:                4      Gaps:          0

US-08-790-043B-2 (1-256) x US-10-089-740-1 (1-39)
QY      1 MetLeuAsnLeuGluAsnLysThrTyrVal 10
Db      10 AUGTTAAATCTTGAAGAAACAAACATATATGTC 39
|||||
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Search completed: September 6, 2005, 14:41:06  
Job time : 704 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: September 6, 2005, 13:10:24 ; Search time 617 Seconds  
(without alignments)  
2717.215 Million cell updates/sec

Title: US-08-790-043B-2  
Perfect score: 256  
Sequence: 1 MLNLENTYVIMGIAKRSL.....LSSGVGTGNIHVDSGFHAIK 256

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Ygapop 60.0 , Ygapext 60.0  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 7338684 seqs, 3274456166 residues

Word size: 1

Total number of hits satisfying chosen parameters: 14665415

Minimum DB seq length: 0  
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-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60  
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :

Published Applications NA:  
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11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:\*  
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26: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	256	100.0	768	9	US-09-815-242-4173	Sequence 4173, Ap
2	256	100.0	771	9	US-09-815-242-8437	Sequence 8437, Ap
3	256	100.0	771	9	US-09-815-242-8794	Sequence 8794, Ap
4	256	100.0	771	17	US-10-282-122A-7734	Sequence 7734, Ap
5	256	100.0	771	21	US-10-857-625-263	Sequence 263, Ap
6	256	100.0	771	21	US-10-888-524-1	Sequence 1, Appl
7	256	100.0	6985	21	US-10-857-625-34	Sequence 34, Appl
8	190	74.2	916	16	US-10-138-701-5	Sequence 5, Appl
9	190	74.2	916	16	US-10-823-785-5	Sequence 5, Appl
10	159	62.1	704	8	US-08-781-986A-772	Sequence 772, App
11	159	62.1	704	18	US-10-329-624-772	Sequence 772, App
c 12	152	59.4	552	9	US-09-815-242-1952	Sequence 1952, Ap
c 13	152	59.4	552	9	US-09-815-242-1963	Sequence 1963, Ap
c 14	152	59.4	552	17	US-10-282-122A-4490	Sequence 4490, Ap
c 15	152	59.4	552	17	US-10-282-122A-4491	Sequence 4491, Ap
c 16	107	41.8	324	9	US-09-815-242-1697	Sequence 1697, Ap
c 17	107	41.8	324	9	US-09-815-242-3050	Sequence 3050, Ap
c 18	107	41.8	324	17	US-10-282-122A-4224	Sequence 4224, Ap
c 19	107	41.8	324	17	US-10-282-122A-5569	Sequence 5569, Ap
c 20	96	37.5	289	9	US-09-815-242-1666	Sequence 1666, Ap
c 21	96	37.5	289	17	US-10-282-122A-4233	Sequence 4233, Ap
c 22	73	28.5	229	9	US-09-815-242-2214	Sequence 2214, Ap
c 23	73	28.5	229	9	US-09-815-242-2218	Sequence 2218, Ap
c 24	73	28.5	229	9	US-09-815-242-2219	Sequence 2219, Ap
c 25	73	28.5	229	9	US-09-815-242-2529	Sequence 2529, Ap
c 26	73	28.5	229	9	US-09-815-242-3421	Sequence 3421, Ap
c 27	73	28.5	229	17	US-10-282-122A-4728	Sequence 4728, Ap
c 28	73	28.5	229	17	US-10-282-122A-4739	Sequence 4739, Ap
c 29	73	28.5	229	17	US-10-282-122A-4747	Sequence 4747, Ap
c 30	73	28.5	229	17	US-10-282-122A-5075	Sequence 5075, Ap
c 31	73	28.5	229	17	US-10-282-122A-5976	Sequence 5976, Ap
c 32	41	16.0	363	17	US-10-282-122A-35143	Sequence 35143, A
c 33	33	12.9	101	9	US-09-815-242-3021	Sequence 3021, Ap
c 34	33	12.9	101	17	US-10-282-122A-5575	Sequence 5575, Ap
c 35	33	12.9	587	8	US-08-781-986A-514	Sequence 514, App
c 36	33	12.9	587	18	US-10-329-624-514	Sequence 514, App
c 37	32	12.5	768	17	US-10-282-122A-34355	Sequence 34355, A
c 38	32	12.5	768	22	US-10-724-972A-2044	Sequence 2044, Ap
c 39	20	7.8	768	17	US-10-282-122A-10473	Sequence 10473, A
c 40	20	7.8	777	17	US-10-369-493-40175	Sequence 40175, A
c 41	19	7.4	102	9	US-09-815-242-2921	Sequence 2921, Ap
c 42	19	7.4	102	17	US-10-282-122A-5478	Sequence 5478, Ap
c 43	15	5.9	780	17	US-10-369-493-43741	Sequence 43741, A
c 44	15	5.9	783	17	US-10-369-493-41051	Sequence 41051, A
c 45	15	5.9	792	17	US-10-369-493-42526	Sequence 42526, A

ALIGNMENTS

RESULT 1

US-09-815-242-4173  
; Sequence 4173, Application US/09815242  
; Patent No. US20020061569A1  
; GENERAL INFORMATION:  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari L.  
; APPLICANT: Zyskind, Judith W.  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John D.  
; APPLICANT: Carr, Grant J.  
; APPLICANT: Yamamoto, Robert T.  
; APPLICANT: Xu, H. Howard  
; TITLE OF INVENTION: Identification of Essential Genes in  
; PROKARYOTES  
; FILE REFERENCE: ELITRA.011A

; CURRENT APPLICATION NUMBER: US/09/815,242  
; CURRENT FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; NUMBER OF SEQ ID NOS: 14110  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4173  
; LENGTH: 768  
; TYPE: DNA  
; ORGANISM: Staphylococcus aureus  
; US-09-815-242-4173

Alignment Scores:  
Pred. No.: 1,89e-256 Length: 768  
Score: 256.00 Matches: 256  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0

US-08-790-043B-2 (1-256) x US-09-815-242-4173 (1-768)

Qy 1 MetLeuAsnLeuGluAsnLysThrTyrValIleMetGlyIleAlaAsnLysArgSerIle 20  
Db 1 ATGTTAAATCTTGAAACAAACAAATATGTCATCGGAATCGCTAATAAGCGTAGTATT 60  
Qy 21 AlaPheGlyValAlaLysValLeuAspGlnLeuGlyAlaLysLeuValPheThrTyrArg 40  
Db 61 GCTTTTGGTGCCTAAAGTTTGTAGATCAATTAGGTGCTAAATTAGTATTACTTACCGT 120  
Qy 41 LysGluArgSerArgLysGluLeuGluLysLeuLeuGluGlnLeuAsnGlnProGluAla 60  
Db 121 AAAGAAGCTAGCGTAAAGCTTGAAAATATTATAGACAAATTAATCAACAGAGCG 180  
Qy 61 HisLeuTyrGlnIleAspValGlnSerAspGluValIleAsnGlyPheGluGlnIle 80  
Db 181 CACTTATATCAAAATTCATGTTCAAGCGATGAAGAAGTTATTAAATGGTTTTCAGCAAAAT 240  
Qy 81 GlyLysAspValGlyAsnIleAspGlyValTyrHisSerIleAlaPheAlaAsnMetGlu 100  
Db 241 GGTAAAGATGTTGGCAATATCGATGCTGTATATCATTCATCGCAATTCCTAATATGGA 300  
Qy 101 AspLeuArgGlyValArgPheSerGluThrSerArgGluGlyPheLeuAlaGlnAspIle 120  
Db 301 GATTTACGGGAGCTTTTCTGAACTTCACGTGAAGGTTCTGTGACCCCAAGACATT 360  
Qy 121 SerSerTyrSerLeuThrIleValAlaHisGluAlaLysLysLeuMetProGluGlyGly 140  
Db 361 AGTTCTTACTCACTAATCTGTTGCTCATGAAGCTAAAAAATTAATGCCAAGAGTGTG 420  
Qy 141 SerIleValAlaThrThrTyrLeuGlyGlyGluPheAlaValGlnAsnTyrAsnValMet 160  
Db 421 AGCATTTGTTGCACAAACATATTTAGTGGCGAATTCGCAGTTCAAACTTACAAATGTGATG 480  
Qy 161 GlyValAlaLysAlaSerLeuGluAlaAsnValLysTyrLeuAlaLeuAspLeuGlyPro 180  
Db 481 GGTGTTGCTTAAGCGAGCTTAGAGCAATGTTAATATATTAGCATTAGCTAGTGTCCA 540  
Qy 181 AspAsnIleArgValAsnAlaIleSerAlaGlyProIleArgThrIleuSerAlaLysGly 200  
Db 541 GATAATATTTCGGTTAATGCAATTTTCAGCTGGTCCCAATCCGTACATTAAAGTGCAAAAGT 600

Qy 201 ValGlyGlyPheAsnThrIleLeuLysGluIleGluGluArgAlaProLeuLysArgIle 220  
Db 601 GTGGGTGGTTTCAATACAAATCTTTAAAGAAATCGAAGAGCGTGCACCTTTAAACGTAAC 660  
Qy 221 ValAspGlnValGluValGlyLysThrAlaAlaTyrLeuLeuSerAspLeuSerSerGly 240  
Db 661 GTTGATCAAGTAGAAGTAGGTAAACACAGCGGCTTACTTATTAAAGTACTTATCAAGTGGC 720  
Qy 241 ValThrGlyGluAsnIleHisValAspSerGlyPheHisAlaIleLys 256  
Db 721 GTTACAGGTGAAAATATTTCATGTAGATAGCGGATTCACGCAATTAATAA 768

#### RESULT 2

US-09-815-242-8437  
; Sequence 8437, Application US/09815242  
; Patent No. US20020061569A1  
; GENERAL INFORMATION:  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari L.  
; APPLICANT: Zyskind, Judith W.  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John D.  
; APPLICANT: Carr, Grant J.  
; APPLICANT: Yamamoto, Robert T.  
; APPLICANT: Xu, H. Howard  
; TITLE OF INVENTION: Identification of Essential Genes in  
; FILE REFERENCE: ELITRA.011A  
; CURRENT APPLICATION NUMBER: US/09/815,242  
; CURRENT FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; NUMBER OF SEQ ID NOS: 14110  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8437  
; LENGTH: 771  
; TYPE: DNA  
; ORGANISM: Staphylococcus aureus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(771)  
US-09-815-242-8437

Alignment Scores:  
Pred. No.: 1.9e-256 Length: 771  
Score: 256.00 Matches: 256  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0

US-08-790-043B-2 (1-256) x US-09-815-242-8437 (1-771)

Qy 1 MetLeuAsnLeuGluAsnLysThrTyrValIleMetGlyIleAlaAsnLysArgSerIle 20  
Db 1 ATGTTAAATCTTGAAACAAACAAATATGTCATCGGAATCGCTAATAAGCGTAGTATT 60  
Qy 21 AlaPheGlyValAlaLysValLeuAspGlnLeuGlyAlaLysLeuValPheThrTyrArg 40  
Db 61 GCTTTTGGTGCCTAAAGTTTTCAGTCAATCAATAGGTGCTAAATTAGTATTACTTACCGT 120











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Qy 121 SerSerTyrSerLeuThrIleValAlaHisGluAlaLysLysLeuMetProGluGlyGly 140
Db 456 AGTTCTTACTCATTAACAATTTGGCTCATGAAGCTAAAAAATTAATGCCAGAAGGTGGT 515
Qy 141 SerIleValAlaThrThrTyrLeuGlyGlyGluPheAlaValGlnAsnTyrAsnValMet 160
Db 516 AGCATTGTGGCAACAATATTTAGGTGGCAATTCGCAGTTCAAACTATATATGTATG 575
Qy 161 GlyValAlaLysAlaSerLeuGluAlaAsnValLysTyrLeuAlaLeuAspLeuGlyPro 180
Db 576 GGTGCTGCTAAAGCGAGCTAGGAAGCAAAATGTTAAATATTTAGCATTAGACTTAGGTCCA 635
Qy 181 AspAsnIleArgValAsnAlaLysSerAlaGly-ProIleArgThrLeuSerAlaLysG1 200
Db 636 GATAAATATTCGCGTTAATGCAATTTCCAGTAG-TCCAATCCGTACATTAAAGTGCAAAAGG 694
Qy 200 YValGlyGlyPheAsnThrIleLeuLysGluIleGluGluArgAlaProLeuLysArgAs 220
Db 695 TGTGGGTGGTTTCNATCAAAATCTTAAAGAAATCGAAGAGCGTGCACCTTTTAAACGTAA 754
Qy 220 nValAspGlnValGluValGlyLysThrAlaAlaTyrLeuLeuSerAspLeuSerSerG1 240
Db 755 TGTTGATCAAGTAGAAGTAGTAAACTGCGGCTTACTTATTAAAGTGAATTTATCAAGTGG 814
Qy 240 YValThrGlyGluAsnIleHisValAspSerGlyPheHisAlaLys 256
Db 815 CGTTACAGGTGAAATATTCATGTAGATAGCGGATTCACGCAATTAATA 863

RESULT 9
US-10-823-785-5
; Sequence 5, Application US/10823785
; Publication No. US20040265962A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc. et al.
; TITLE OF INVENTION: Staphylococcus aureus genes and polypeptides
; FILE REFERENCE: PB484
; CURRENT APPLICATION NUMBER: US/10/823,785
; PRIOR FILING DATE: 2004-04-14
; PRIOR APPLICATION NUMBER: US/09/512,255
; PRIOR FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: US 60/098,964
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: US 60/009,861
; PRIOR FILING DATE: 1996-01-05
; PRIOR APPLICATION NUMBER: PCT/ US99/19726
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: US 08/956,171
; PRIOR FILING DATE: 1997-10-20
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 916
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-823-785-5

Alignment Scores:
Pred. No.: 1.23e-187 Length: 916
Score: 190.00 Matches: 255
Percent Similarity: 99.22% Conservative: 0
Best Local Similarity: 99.22% Mismatches: 1
Query Match: 74.22% Indels: 2
DB: 20 Gaps: 0

US-08-790-043B-2 (1-256) x US-10-823-785-5 (1-916)
Qy 1 MetLeuAsnLeuGluAsnLysThrTyrValIleMetGlyIleAlaAsnLysArgSerIle 20
Db 96 ATGTTAAATCTTGAAACAAACATATGTATCATCGGAATCGTAAGCGTAGTATT 155
Qy 21 AlaPheGlyValAlaLysValLeuAspGlnLeuGlyAlaLysLeuValPheThrTyrArg 40
Db 156 GCTTTTGGTGTGCTAAAGTTTATGATCAATAGGTGCTAAATTAGTATTACTTACCGGT 215
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Qy 41 LysGluArgSerArgLysGluLeuGluLysLeuLeuGluGlnLeuAsnGlnProGluAla 60
Db 216 AAAGAAGCTAGCGGTAAAGAGCTTGAAATAATTTATAGAACAAATTAATCAACCAAGCG 275
Qy 61 HisLeuTyrGlnIleAspValGlnSerAspGluGluValIleAsnGlyPheGluGlnIle 80
Db 276 CACTTATATCAAAATTCATGTTCAAGCGATGAAGAGGTTATTAAATGGTTTTAGCAAAAT 335
Qy 81 GlyLysAspValGlyAsnIleAspGlyValTyrHisSerIleAlaPheAlaAsnMetGlu 100
Db 336 GGTAAAGATGTTGGCAATATTTGATGTTATATCATTCATTCGATTTGCTATATATGGA 395
Qy 101 AspLeuArgGlyArgPheSerGluThrSerArgGluGlyPheLeuLeuAlaGlnAspIle 120
Db 396 GACTTACCGGACGCTTTTCTGAAACTTCACGTTGAAGGCTTCTTGTAGTCAAGACATT 455
Qy 121 SerSerTyrSerLeuThrIleValAlaHisGluAlaLysLysLeuMetProGluGlyGly 140
Db 456 AGTTCTTACTCATTAACAATTTGGCTCATGAAGCTAAAAAATTAATGCCAGAAGGTGGT 515
Qy 141 SerIleValAlaThrThrTyrLeuGlyGlyGluPheAlaValGlnAsnTyrAsnValMet 160
Db 516 AGCATTGTGGCAACAATATTTAGGTGGCAATTCGCAGTTCAAACTATATATGTATG 575
Qy 161 GlyValAlaLysAlaSerLeuGluAlaAsnValLysTyrLeuAlaLeuAspLeuGlyPro 180
Db 576 GGTGTTGCTTAAAGCGAGCTTAGAAGCAAAATGTTAAATATTTAGCATTAGACTTAGGTCCA 635
Qy 181 AspAsnIleArgValAsnAlaLysSerAlaGly-ProIleArgThrLeuSerAlaLysG1 200
Db 636 GATAAATATTCGCGTTAATGCAATTTCCAGTAG-TCCAATCCGTACATTAAAGTGCAAAAGG 694
Qy 200 YValGlyGlyPheAsnThrIleLeuLysGluIleGluGluArgAlaProLeuLysArgAs 220
Db 695 TGTGGGTGGTTTCATCAAAATCTTAAAGAAATCGAAGAGCGTGCACCTTTTAAACGTAA 754
Qy 220 nValAspGlnValGluValGlyLysThrAlaAlaTyrLeuLeuSerAspLeuSerSerG1 240
Db 755 TGTTGATCAAGTAGAAGTAGTAAACTGCGGCTTACTTATTAAAGTGAATTTATCAAGTGG 814
Qy 240 YValThrGlyGluAsnIleHisValAspSerGlyPheHisAlaLys 256
Db 815 CGTTACAGGTGAAATATTCATGTAGATAGCGGATTCACGCAATTAATA 863

RESULT 10
US-08-781-986A-772
; Sequence 772, Application US/08781986A
; Publication No. US20030054436A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
```

```
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PB248PP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 772:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 704 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
;
US-08-781-986A-772

Alignment Scores:
Pred. No.: 1,86e-155 Length: 704
Score: 159.00 Matches: 189
Percent Similarity: 98.95% Conservatives: 0
Best Local Similarity: 98.95% Mismatches: 1
Query Match: 62.11% Indels: 2
DB: 8 Gaps: 0

US-08-790-043B-2 (1-256) x US-08-781-986A-772 (1-704)

QY 1 MetLeuAsnLeuGluAsnLysThrTyrValIleMetGlyIleAlaAsnLysArgSerIle 20
DB 24 ATGTTAAATCTTGAACAACAAACATATGTCATGGGAATCGCTAATGAAGCGTAGTATT 83
QY 21 AlaPheGlyValAlaLysValLeuAspGlnLeu-GlyAlaLysLeuValPheThrTyrAr 40
DB 84 GCTTTTGGTGTGCTAAAGTTTGTAGATCAATT-MGGTGTCTAAATTAGTATTACTTACCG 142
QY 40 glysGluArgSerArgLysGluLeuGlnLysLeuLeuGlnLeuAsnGlnProGluAl 60
DB 143 TAAAGAACGTAGCCGTAAGAGCTTGAAAAATTTATTAGAACCAATTAATAATCAACCAAGC 202
QY 60 ahisLeuTyrGlnIleAspValGlnSerAspGluGluValIleAsnGlyPheGluGlnI 80
DB 203 GCACCTTATATCAATTTGATGTTCAAGCGATGAGAGGTTTATTATGTTTGGACCAAT 262
QY 80 eGlyLysAspValGlyAsnIleAspGlyValTyrHisSerIleAlaPheAlaAsnMetGl 100
DB 263 TGTAAAGATGTTGGCAATATTGATGGTGTATATCAATCGCATTTGCTTAATATGGA 322
QY 100 uasplLeuArgGlyArgPheSerGluThrSerArgGluGlyPheLeuLeuAlaGlnAspI 120
DB 323 AGACTTTACCGGACGCGCTTTTCTGAAACTTTCACGTGAAGCGCTTCTTTGTAGCTCAAGACAT 382
QY 120 eSerSerTyrSerLeuThrIleValAlaHisGluAlaLysLysLeuMetProGluGlyGl 140
DB 383 TAGTCTTACTCATTTACCAATTTGTGGCTCATGAGCTAAAAATTAATGCCAAGAGGTGG 442
QY 140 ySerIleValAlaThrThrTyrLeuGlyGlyGluPheAlaValGlnAsnTyrAsnValMe 160
DB 443 TAGCATTTGTTCAACAACAATATTATTAGTGGCGAAATTCGCAGTTTCAAACTATAATGTGAT 502
QY 160 tGlyValAlaLysAlaSerLeuGluAlaAsnValLysTyrLeuAlaLeuAspLeuGlyPr 180
DB 503 GGGTGTGTGTTAAAGCGAGCTTGAAGCAATATTGTAATATTTTAGCATTTAGCACTTAGGTCC 562
QY 180 oAspAsnIleArgValAsnAlaIleSerAla 190
DB 563 AGATAATATTCGGTTTAAATTCACATTTTCAGCT 593
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RESULT 11
US-10-329-624-772
; Sequence 772, Application US/10329624
; Publication No. US2004004307A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; Gil H. Choi
; Patrick S. Dillon
; Craig A. Rosen
```

```
; Steven C. Barash
; Michael R. Fannon
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5256
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
;
COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/329,624
; FILING DATE: 27-Dec-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/956,171
; FILING DATE: October 20, 1997
; APPLICATION NUMBER: 60/009,861
; FILING DATE: January 5, 1996
; APPLICATION NUMBER: 08/781,986
; FILING DATE: January 3, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mark J. Hyman
; REGISTRATION NUMBER: 46,789
; REFERENCE/DOCKET NUMBER: PB248PID1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (240) 314-1224
; TELEFAX: (301) 309-8439
; INFORMATION FOR SEQ ID NO: 772:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 704 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 772:
;
US-10-329-624-772
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Alignment Scores:
Pred. No.: 1,86e-155 Length: 704
Score: 159.00 Matches: 189
Percent Similarity: 98.95% Conservatives: 0
Best Local Similarity: 98.95% Mismatches: 1
Query Match: 62.11% Indels: 2
DB: 18 Gaps: 0

US-08-790-043B-2 (1-256) x US-10-329-624-772 (1-704)

QY 1 MetLeuAsnLeuGluAsnLysThrTyrValIleMetGlyIleAlaAsnLysArgSerIle 20
DB 24 ATGTTAAATCTTGAACAACAAACATATGTCATCGGAATCGCTAATAAGCGTAGTATT 83
QY 21 AlaPheGlyValAlaLysValLeuAspGlnLeu-GlyAlaLysLeuValPheThrTyrAr 40
DB 84 GCTTTTGGTGTGCTAAAGTTTGTAGATCAATT-MGGTGTCTAAATTAGTATTACTTACCG 142
QY 40 glysGluArgSerArgLysGluLeuGlnLysLeuLeuGlnLeuAsnGlnProGluAl 60
DB 143 TAAAGAACGTAGCCGTAAGAGCTTGAAAAATTTATTAGAACCAATTAATAATCAACCAAGC 202
QY 60 ahisLeuTyrGlnIleAspValGlnSerAspGluGluValIleAsnGlyPheGluGlnI 80
DB 203 GCACCTTATATCAATTTGATGTTCAAGCGATGAGAGGTTTATTATGTTTGGACCAAT 262
QY 80 eGlyLysAspValGlyAsnIleAspGlyValTyrHisSerIleAlaPheAlaAsnMetGl 100
DB 263 TGTAAAGATGTTGGCAATATTGATGGTGTATATCAATCGCATTTGCTTAATATGGA 322
QY 100 uasplLeuArgGlyArgPheSerGluThrSerArgGluGlyPheLeuLeuAlaGlnAspI 120
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Db 323 AGCTTACGGCGAGCTTTCTTGAAGAACTTCACGTGAAGGCTTCTGTGTAGCTCAAGACAT 382  
Qy 120 eSerSerTyrSerLeuThrIleValAlaHisGluAlaLysLysLeuMetProGluGlyG1 140  
Db 383 TAGTCTTACTCATTAACAATTTGGGCTCATGAAGCTTAAAAATTAATGCGAGAGTGG 442  
Qy 140 ySerIleValAlaThrThrTyrLeuGlyGlyGluPheAlaValAlaValAlaValAlaValMe 160  
Db 443 TAGCATTTGTTGCAACAACATATTTAGGTGGCGAATTCGCGAGTTCAAAACTATAATGTGAT 502  
Qy 160 tGlyValAlaValAlaSerLeuGluAlaAsnValLysTyrLeuAlaLeuAspLeuGlyPr 180  
Db 503 GGGTGTGCTTAAGCGAGCTTAGAAGCAATGTTAAATATTTAGCATTTAGACTTAGGTCC 562  
Qy 180 oAspAsnIleArgValAlaAlaIleSerAla 190  
Db 563 AGATAATATTCGCGTTAATGCAATTTTCAGCT 593

RESULT 12  
US-09-815-242-1952/c  
; Sequence 1952, Application US/09815242  
; Patent No. US20020061569A1  
; GENERAL INFORMATION:  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari L.  
; APPLICANT: Zyskind, Judith W.  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John D.  
; APPLICANT: Carr, Grant J.  
; APPLICANT: Yamamoto, Robert T.  
; APPLICANT: Xu, H. Howard  
; TITLE OF INVENTION: Identification of Essential Genes in  
; FILE REFERENCE: ELITRA.011A  
; CURRENT APPLICATION NUMBER: US/09/815,242  
; CURRENT FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; NUMBER OF SEQ ID NOS: 14110  
; SOFTWARE: Fast-SEQ for Windows Version 4.0  
; SEQ ID NO 1952  
; LENGTH: 552  
; TYPE: DNA  
; ORGANISM: Staphylococcus aureus

US-09-815-242-1952  
Alignment Scores:  
Pred. No.: 2,9e-148 Length: 552  
Score: 152.00 Matches: 152  
Percent Similarity: 100.00% Conservativeness: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 59.38% Indels: 0  
DB: 9 Gaps: 0

US-08-790-043B-2 (1-256) x US-09-815-242-1952 (1-552)  
Qy 1 MetLeuAsnLeuGluAsnLysThrTyrValIleMetGlyIleAlaAsnLysArgSerile 20  
Db 456 ATGTTAAATCTTGAAAACAAAACATATGTCATCTGGGAATCGTAAATAGCGTAGTATT 397

Qy 21 AlaPheGlyValAlaLysValLeuAspGlnLeuGlyAlaLysLeuValPheThrTyrArg 40  
Db 396 GCTTTTGGTGTCTGCTAAAGTTTTAGATCAATTAGGTCTAAATTAGTATTACTTACCGT 337  
Qy 41 LysGluArgSerArgLysGluLeuGlyLysLeuGluGlnLeuAsnGlnProGluAla 60  
Db 336 AAGAAGCGTAGCGGTAAAGAGCTTGAATAATTAATAGAACAAATAAATCAACGAGCG 277  
Qy 61 HisLeuTyrGlnIleAspValGlnSerAspGluValIleAsnGlyPheGluGlnIle 80  
Db 276 CACTTATATCAATTCATGTTCAAGCGATGAAGAGGTTATTAAATGGTTTGAGCAAAAT 217  
Qy 81 GlyLysAspValGlyAsnIleAspGlyValTyrHisSerIleAlaPheAlaAsnMetGlu 100  
Db 216 GGTAAAGATGTTGGCAATATTGATGTGTATATCATTCATCAATGCAATTTGCTAATATGGA 157  
Qy 101 AspLeuArgGlyArgPheSerGluThrSerArgGluGlyPheLeuLeuAlaGlnAspIle 120  
Db 156 GACTTACGGCGAGCTTTTCTGAAACTTCACGTGAAGGCTTCTTGTAGCTCAAGACAT 97  
Qy 121 SerSerTyrSerLeuThrIleValAlaHisGluAlaLysLysLeuMetProGluGlyGly 140  
Db 96 AGTTCCTTACTCATTAACAATTTGGGCTCATGAAGCTAAAAAATAATGCCAGAGGTGT 37  
Qy 141 SerIleValAlaThrThrTyrLeuGlyGlyGluPhe 152  
Db 36 AGCATTTGTTGCAACACACATATTTAGGTGGCAATTC 1

RESULT 13  
US-09-815-242-1963/c  
; Sequence 1963, Application US/09815242  
; Patent No. US20020061569A1  
; GENERAL INFORMATION:  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari L.  
; APPLICANT: Zyskind, Judith W.  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John D.  
; APPLICANT: Carr, Grant J.  
; APPLICANT: Yamamoto, Robert T.  
; APPLICANT: Xu, H. Howard  
; TITLE OF INVENTION: Identification of Essential Genes in  
; FILE REFERENCE: ELITRA.011A  
; CURRENT APPLICATION NUMBER: US/09/815,242  
; CURRENT FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; NUMBER OF SEQ ID NOS: 14110  
; SOFTWARE: Fast-SEQ for Windows Version 4.0  
; SEQ ID NO 1963  
; LENGTH: 552  
; TYPE: DNA  
; ORGANISM: Staphylococcus aureus

US-09-815-242-1963  
Alignment Scores:  
Pred. No.: 2,9e-148 Length: 552  
Score: 152.00 Matches: 152  
Percent Similarity: 100.00% Conservativeness: 0  
Best Local Similarity: 100.00% Mismatches: 0

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Query Match: 59.38% Indels: 0
DB: 9 Gaps: 0
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DB 456 ATGTTAAATCTTGAAACAACAACATATGTCATCATGGGAATGCTAATAAGCGTAGTATT 397
QY 21 AlaPheGlyValAlaLysValLeuAspGlnLeuGlyAlaLysLeuValPheThrTyrArg 40
DB 396 GCTTTTGGTGCCTAAAGTTTAGATCAATTAGGTGCTAAATTAGTATTACTTTACCGT 337
QY 41 LysGluArgSerArgLysGluLeuGlyLysLeuGluGlnLeuAsnGlnProGluAla 60
DB 336 AAAGAACGTAGCGGTAAAGAGCTTGAAATAATATTAGAACAAATTAATCAACCAAGGCG 277
QY 61 HisLeuTyrGlnIleAspValGlnSerAspGluGluValIleAsnGlyPheGluGlnIle 80
DB 276 CACTTATATCAAAATGATGTTCAAGCGATGAAGAGGTATTAAATGGTTTGGAGCAAT 217
QY 81 GlyLysAspValGlyAenLysLeuAspGlyValTyrHisSerileAlaPheAlaAenMetGlu 100
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DB 156 GACTTACGCGGACGCTTTTCTGAAACTTCACGTGAAGGCTTCTTGTAGCTCAAGACAT 97
QY 121 SerSerTyrSerLeuThrIleValAlaHisGluAlaLysLysLeuMetProGluGlyGly 140
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QY 141 SerIleValAlaThrThrTyrLeuGlyGlyGluPhe 152
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RESULT 14
US-10-282-122A-4490/c
; Sequence 4490, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; FILE OF INVENTION: Identification of Essential Genes in Microorganisms
; TITLE REFERENCE: ELITRA 034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
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; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4490
; LENGTH: 552
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-282-122A-4490
Alignment Scores:
Pred. No.: 2.9e-148 Length: 552
Score: 152.00 Matches: 152
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 59.38% Indels: 0
DB: 17 Gaps: 0
US-08-790-043B-2 (1-256) x US-10-282-122A-4490 (1-552)
QY 1 MetLeuAsnLeuGluAenLysThrTyrValIleMetGlyVileAlaAenLysArgSerile 20
DB 456 ATGTTAAATCTTGAAACAACAACATATGTCATCATGGGAATCGCTAATAAGCGTAGTATT 397
QY 21 AlaPheGlyValAlaLysValLeuAspGlnLeuGlyAlaLysLeuValPheThrTyrArg 40
DB 396 GCTTTTGGTGCCTAAAGTTTAGATCAATTAGGTGCTAAATTAGTATTACTTTACCGT 337
QY 41 LysGluArgSerArgLysGluLeuGlyLysLeuGluGlnLeuAsnGlnProGluAla 60
DB 336 AAAGAACGTAGCGGTAAAGAGCTTGAAATAATATTAGAACAAATTAATCAACCAAGGCG 277
QY 61 HisLeuTyrGlnIleAspValGlnSerAspGluGluValIleAsnGlyPheGluGlnIle 80
DB 276 CACTTATATCAAAATGATGTTCAAGCGATGAAGAGGTATTAAATGGTTTGGAGCAAT 217
QY 81 GlyLysAspValGlyAenLysLeuAspGlyValTyrHisSerileAlaPheAlaAenMetGlu 100
DB 216 GGTAAAGATGTTGGCAATATTGATGCTATATCAATCGCATTTGCTAATAATGGAA 157
QY 101 AspLeuArgLysArgPheSerGluThrSerArgGluGlyPheLeuLeuAlaGlnAspIle 120
DB 156 GACTTACGCGGACGCTTTTCTGAAACTTCACGTGAAGGCTTCTTGTAGCTCAAGACAT 97
QY 121 SerSerTyrSerLeuThrIleValAlaHisGluAlaLysLysLeuMetProGluGlyGly 140
DB 96 AGTTCTTACTCATTAACAATTTGGCTCATGAAGCTAAAAAATTAATGCCAAGGTGGT 37
QY 141 SerIleValAlaThrThrTyrLeuGlyGlyGluPhe 152
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US-10-282-122A-4491/c
; Sequence 4491, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
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; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282.122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
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; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4491
; LENGTH: 552
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
; US-10-282-122A-4491

Alignment Scores:

Pred. No.: 2,9e-148 Length: 552
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DB: 17 Gaps: 0

US-08-790-043B-2 (1-256) x US-10-282-122A-4491 (1-552)

Qy 1 MetLeuAsnLeuGluAsnLysThrTyrValIleMetGlyIleAlaAsnLysArgSerIle 20
Db 456 ATGTTAAATCTGAAAAACAAACATATGTCATCGGAATCGCTAATAAGCGTAGTATT 397
Qy 21 AlapheGlyValAlaLysValLeuAspGlnLeuGlyAlaLysLeuValPheThrTyrArg 40
Db 396 GCTTTTGGTGTGCGTAAAGTTTATAGATCAATTAGGTGCTAAATTAGTATTCTTACCGT 337
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Db 336 AAAGAAGTACCGCTAAGAGCTTGAAAAATTTATTAGAACATTAATCAACCCAGAGCG 277
Qy 61 HisLeuTyrGlnIleAspValGlnSerAspGluValIleAsnGlyPheGluGlnIle 80
Db 276 CACTTATATCAATTGATGTTCAAAGCGATGAGAGGTTATTAAATGTTTGGACAAATT 217
Qy 81 GlyLysAspValGlyAsnIleAspGlyValTyrHisSerIleAlaPheAlaAsnMetGlu 100
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Db 156 GACTTACCGGACGCTTTTCTGAACCTTCAGTGAAGGCTTCTTGTAGCTCAAGACATT 97
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Search completed: September 6, 2005, 16:18:17  
Job time : 624 secs

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